

Result No.	Score	Query Match	Length	DB ID	Description
1	177.5	19.6	181	4	US-09-752-991A-21217 Sequence 21217, A
2	161	17.8	183	4	US-09-543-681A-6409 Sequence 6409, App
3	14.5	14.9	197	3	US-08-936-408-2 Sequence 2, Appli
4	14.5	14.9	197	3	US-09-310-847-2 Sequence 2, Appli
5	14.5	14.9	197	3	US-09-310-845-2 Sequence 2, Appli
6	14.5	14.9	197	4	US-08-938-023-2 Sequence 2, Appli
7	13.5	14.8	186	4	US-09-448-039A-12407 Sequence 12407, A
8	12.2	13.5	443	2	US-08-795-415-6 Sequence 6, Appli
9	11.8	13.1	382	4	US-09-810-729-206 Sequence 206, APP
10	11.8	13.1	158	4	US-09-119-452A-315 Sequence 315, APP
11	11.0	12.2	8991	4	US-08-714-741-32 Sequence 32, Appli
12	10.5	12.0	955	1	US-08-006-676B-1 Sequence 1, Appli
13	10.5	12.0	955	2	US-08-282-845-2 Sequence 2, Appli
14	10.5	12.0	955	5	PCT-US54-00324-1 Sequence 3, Appli
15	10.5	12.0	955	6	Patent No. 5210183 Patent No. 5210183
16	10.7	11.8	683	6	5210183-3 Sequence 76, Appli
17	10.7	11.8	683	7	5210183-3 Sequence 2, Appli
18	102.5	11.3	708	3	US-08-235-846C-76 Sequence 2, Appli
19	101.5	11.2	700	1	US-07-720-569-2 Sequence 2, Appli
20	101.5	11.2	700	2	US-08-785-190-2 Sequence 2, Appli
21	101.5	11.2	700	3	US-08-743-816C-66 Sequence 66, Appli
22	101.5	11.2	700	5	PCT-US52-05539-2 Sequence 2, Appli
23	101.5	11.2	1972	4	US-08-975-435B-4 Sequence 4, Appli
24	101	11.2	1939	4	US-09-110-187A-1 Sequence 1, Appli
25	10.5	11.1	187	4	US-09-328-728-2 Sequence 7281, Ap
26	10.5	11.1	391	4	US-09-800-729-208 Sequence 208, App
27	10.5	11.1	468	4	US-09-328-352-6321 Sequence 4744, Ap

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 OM protein - protein search, using sw mode
 Run on: April 27, 2004, 09:34:33 ; Search time 22 Seconds
 (without alignments)
 436.474 Million cell updates/sec

Title: US-10-018-290A-1
 Perfect score: 904
 Sequence: 1 MKVKTLSMALLACLVANSA.....INAAWKGGSKLDEMANRKK 186

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgns_6/podata/2/iaa/5A_COMBO_PEP:
 2: /cgns_6/podata/2/iaa/5B_COMBO_PEP:
 3: /cgns_6/podata/2/iaa/6A_COMBO_PEP:
 4: /cgns_6/podata/2/iaa/6B_COMBO_PEP:
 5: /cgns_6/podata/2/iaa/PCTNS_COMBO_PEP:
 6: /cgns_6/podata/2/iaa/backfile1.PEP:
 * Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the result being printed.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	177.5	19.6	181	4	US-09-752-991A-21217 Sequence 21217, A
2	161	17.8	183	4	US-09-543-681A-6409 Sequence 6409, App
3	14.5	14.9	197	3	US-08-936-408-2 Sequence 2, Appli
4	14.5	14.9	197	3	US-09-310-847-2 Sequence 2, Appli
5	14.5	14.9	197	3	US-09-310-845-2 Sequence 2, Appli
6	14.5	14.9	197	4	US-08-938-023-2 Sequence 2, Appli
7	13.5	14.8	186	4	US-09-448-039A-12407 Sequence 12407, A
8	12.2	13.5	443	2	US-08-795-415-6 Sequence 6, Appli
9	11.8	13.1	382	4	US-09-810-729-206 Sequence 206, APP
10	11.8	13.1	158	4	US-09-119-452A-315 Sequence 315, APP
11	11.0	12.2	8991	4	US-08-714-741-32 Sequence 32, Appli
12	10.5	12.0	955	1	US-08-006-676B-1 Sequence 1, Appli
13	10.5	12.0	955	2	US-08-282-845-2 Sequence 2, Appli
14	10.5	12.0	955	5	PCT-US54-00324-1 Sequence 3, Appli
15	10.5	12.0	955	6	Patent No. 5210183 Patent No. 5210183
16	10.7	11.8	683	7	5210183-3 Sequence 76, Appli
17	10.7	11.8	683	8	5210183-3 Sequence 2, Appli
18	102.5	11.3	708	3	US-08-235-846C-76 Sequence 2, Appli
19	101.5	11.2	700	1	US-07-720-569-2 Sequence 2, Appli
20	101.5	11.2	700	2	US-08-785-190-2 Sequence 2, Appli
21	101.5	11.2	700	3	US-08-743-816C-66 Sequence 66, Appli
22	101.5	11.2	700	5	PCT-US52-05539-2 Sequence 2, Appli
23	101.5	11.2	1972	4	US-08-975-435B-4 Sequence 4, Appli
24	101	11.2	1939	4	US-09-110-187A-1 Sequence 1, Appli
25	10.5	11.1	187	4	US-09-328-728-2 Sequence 7281, Ap
26	10.5	11.1	391	4	US-09-800-729-208 Sequence 208, App
27	10.5	11.1	468	4	US-09-328-352-6321 Sequence 4744, Ap

ALIGNMENTS

RESULT 1
 US-09-252-991A-21217 ; Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenstein et al.
 ; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252-991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074-788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOs: 33142
 ; SEQ ID NO 21217
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-21217

Query Match 19.6%; Score 177.5; DB 4;
 Best Local Similarity 30.5%; Pred. No. 9.4e-10;
 Matches 51; Conservative 37; Mismatches 10; Indels 9; Gaps 4;

Qy 5 TLMMAILACLVANSFAADPPIGVNSQSTAMEESPAAKAQKLUQSEFG--NEXTQLE 61
 Db 18 TQFLVLTAAITMAAPASF-AEMKIAVNYQALLESDAAKQYAVDAEKKFQPOLNKLNL 76
 Qy 62 KQAKD1QTKADDLQAKSAAMSNOAREDQKREFLELRRNFEKSRDFAIRVEQANTLRQY 121
 Db 77 RDAKALQ--DKLVSGNSKMSQGDREKAELDFQKARDFOQSKEINESKAADRDMLKK 133

Qy 122 LAEQYIYAAETTAKKGLKLVLDSAGSNTYLEKNLDTIEILEAIN 168
 Db 134 LKPRLDQAVETTIRGGYDVMIE-RGAVYDVDPQYDITRQVIRMN 178

RESULT 2
 US-09-543-681A-6409 ; Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRA
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709-100-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706
 PRIOR FILING DATE: 1999-04-09
 SEQ ID NO: 6409
 LENGTH: 183
 TYPE: PRT
 ORGANISM: Proteus mirabilis
 US-09-543-681A-6409

Query Match 17.8%; Score 161; DB 4; Length 183;
 Best Local Similarity 26.2%; Pred. No. 3.8e-08;
 Matches 44; Conservative 40; Mismatches 74; Indels 10; Gaps 4;

Qy 4 KTLMSMIAILCLVANSAFSADPFIGVNSQIAMESAAKAQKLUQSEFGNEKTOLEKQ 63
 Db 21 KLLCAALGMALMTMSAGQAQADKVGVINIGQVLQRVNDAVEQLLNEFGRDTEQNL 80

Qy 64 AKDLQTAKDDLOQAKSAMNSQAREDQKREFLEURRNEEKS---RDFAIRVEQAENTLR 119
 Db 81 GRALQTAVEKYQKDAPTMNATQANTBDLVAKREAYAQQAQAFEQFSRR-QAEH-R 136

Qy 120 QYLAEQIYLAETIAIACKKGKLVLDSASGSVMYLEKNDITRILEMI 167
 Db 137 NCIMKRVLDLDAVAKCEGYDYLDA-ANTVBYFADDKRDITAQVQKQY 182

RESULT 3
 US-08-996-008-2
 Sequence 2, Application US/08996408
 Patent No. 6245338

GENERAL INFORMATION:
 APPLICANT: Kyd, Jemelle
 APPLICANT: Cripps, Allan
 APPLICANT: Smith, Christopher
 APPLICANT: Pennie & Edmonds LLP
 TITLE OF INVENTION: PEPTIDE LIBRARIES AS A SOURCE OF SYNGENES
 NUMBER OF SEQUENCES: 5
 ADDRESS: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/310,847
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/996,408
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB96/01549
 FILING DATE: 27-JUN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9513074.6
 FILING DATE: 27-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Baldwin, Geraldine F.
 REGISTRATION NUMBER: 31,232
 REFERENCE/DOCKET NUMBER: 7116-068
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEFAX: 212-869-8864
 TELLEX: 66141 PENNIE 2:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 197 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-310-847-2

Query Match 14.9%; Score 134.5; DB 3; Length 197;
 Best Local Similarity 26.8%; Pred. No. 1.6e-05;
 Matches 56; Conservative 34; Mismatches 78; Indels 41; Gaps 7;

QY 2 KVKTLSMALLACLVANSAFSADFPVGNSQSTAMESAAKAAQKKLQSEFGNEKTCOLE 61
 Db 6 KVTTALAGI---ALASGYASAEKKIAFAFINAGYFOHHFDRQAVADKLDAEFKPVAEKLIA 61
 Db 62 KQAKDLOTK---ADDLQAKSAAMSNOAREDKO-----REFLELRNPFEE 102
 QY 62 ASKKEVDDKIAAARKKVKVAALBDAPRLRADIQKRQEETNLGAEDASLQKLMQE 121
 Db 62 KSRPFAIRVEQAENTLRO----YLAEQTYLAETIAKKGKLKVLDASGSYMLEKNL 157
 QY 103 KSDPFAIRVEQAENTLRO----YLAEQYIYLAAETIAKKGKLKVLDASGSYMLEKNL 157
 Db 122 --QDKKVVQFQAQNENKRAEERGLLDSQTATNNLARAKGTYVLD--ANSVVFAVEGK 177
 QY 158 DITKEILLEAINAAWKGGSKLPENANRK 186
 Db 178 DITTEEVLSIPAS-----EKAQEK 197

RESULT 5
 US-09-548-023-2
 ; Sequence 2, Application US/09548023
 ; Patent No. 6311281
 ; GENERAL INFORMATION:
 ; APPLICANT: Kyd, Janelle Cripps, Allan Smith, Christopher Smith,
 ; APPLICANT: Crippe, Allian
 ; APPLICANT: Smith, Christopher
 ; TITLE OF INVENTION: PEPTIDE LIBRARIES AS A SOURCE OF SYNGENES
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/548,023
 ; FILING DATE: 12-Apr-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/996,408
 ; FILING DATE: 27-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Baldwin, Geraldine F.
 ; REGISTRATION NUMBER: 31,232
 ; TELECOMMUNICATION INFORMATION:
 ; APPLICATION NUMBER: GB 9513074.6
 ; FILING DATE: 27-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Baldwin, Geraldine F.
 ; REGISTRATION NUMBER: 7116-068
 ; TELEPHONE: 212-790-9090
 ; TELEX: 66141 PENNIE 2:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 197 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-548-023-2

Query Match 14.9%; Score 134.5; DB 3; Length 197;
 Best Local Similarity 26.8%; Pred. No. 1..e-05;
 Matches 56; Conservative 34; Mismatches 78; Indels 41; Gaps 7;

QY 2 KVKTLSMALLACLVANSAFSADFPVGNSQSTAMESAAKAAQKKLQSEFGNEKTCOLE 61
 Db 6 KVTTALAGI---ALASGYASAEKKIAFAFINAGYFOHHFDRQAVADKLDAEFKPVAEKLIA 61
 Qy 62 KQAKDLOTK---ADDLQAKSAAMSNOAREDKO-----REFLELRNPFEE 102
 Db 62 ASKKEVDDKIAAARKKVKVAALBDAPRLRADIQKRQEETNLGAEDASLQKLMQE 121
 Qy 103 KSRPFAIRVEQAENTLRO----YLAEQTYLAETIAKKGKLKVLDASGSYMLEKNL 157
 Db 122 --QDKKVVQFQAQNENKRAEERGLLDSQTATNNLARAKGTYVLD--ANSVVFAVEGK 177
 Qy 158 DITKEILLEAINAAWKGGSKLPENANRK 186
 Db 178 DITTEEVLSIPAS-----EKAQEK 197

RESULT 6
 US-09-548-023-2
 ; Sequence 2, Application US/09548023
 ; Patent No. 6311281
 ; GENERAL INFORMATION:
 ; APPLICANT: Kyd, Janelle Cripps, Allan Smith, Christopher Smith,
 ; APPLICANT: Crippe, Allian
 ; APPLICANT: Smith, Christopher
 ; TITLE OF INVENTION: PEPTIDE LIBRARIES AS A SOURCE OF SYNGENES
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/548,023
 ; FILING DATE: 12-Apr-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/996,408
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Baldwin, Geraldine F.
 ; REGISTRATION NUMBER: 31,232
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: <Unknown>
 ; TELEX: 66141 PENNIE 2:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 197 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 ; US-09-548-023-2

Query Match 14.9%; Score 134.5; DB 4; Length 197;
 Best Local Similarity 26.8%; Pred. No. 1..e-05;
 Matches 56; Conservative 34; Mismatches 78; Indels 41; Gaps 7;

Qy 2 KVKTLSMALLACLVANSAFSADFPVGNSQSTAMESAAKAAQKKLQSEFGNEKTCOLE 61
 Db 6 KVTTALAGI---ALASGYASAEKKIAFAFINAGYFOHHFDRQAVADKLDAEFKPVAEKLIA 61
 Qy 62 KQAKDLOTK---ADDLQAKSAAMSNOAREDKO-----REFLELRNPFEE 102

RESULT 7
 US-09-489-039A-12407
 ; Sequence 12407, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; FILE REFERENCE: 2709.004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; PRIORITY FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO: 12407
 ; LENGTH: 186
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae
 ;US-09-489-039A-12407

Query Match 14.8%; Score 133.5; DB 4; Length 186;
 Best Local Similarity 25.3%; Pred. No. 1.8e-05;
 Matches 42; Conservative 38; Mismatches 79; Indels 7; Gaps 4;

Qy 3 VKTLSMALLACLVANSFAFSADPFGVENSOSTAMESAAAKQKLQSEFGNNEKTLQEK 62
 Db 26 VKKWLLAAGLGLAMTSQAAD-KIAVNNVNSLFFQQAQTKGVSNTLEENFKGRASELQR 84

Qy 63 QAKDILQTKADDIQLQKIAAMSNOAREDQREFELRNFEKSRSDFAIRVEOAENTRQYL 122
 Db 85 MBGDLSRSMQQLSRSMGAB --RTKLEKDMDAQRTQFSQAAFFQDRARRSNEERGKL 141

Qy 123 AEQIVYIAAETIATKKIGKLVLDSASGSVMMLEKNL-DITRILEAI 167
 Db 142 VTRIQTAQSVAKDQSTDLYVD--ANAVATNSSDVDTITADVLQV 185

RESULT 8
 US-08-795-475-6
 ; Sequence 6, Application US/08795475
 ; Patent No. 5965390
 ; GENERAL INFORMATION:
 ; APPLICANT: Björck, Lars
 ; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104-1792
 ; COMPUTER: IBM PC compatible
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/795,475
 ; FILING DATE: 11-FEB-1997

Query Match 13.1%; Score 118.5; DB 4; Length 382;
 Best Local Similarity 26.8%; Pred. No. 0.0014;
 Matches 34; Conservative 29; Mismatches 47; Indels 17; Gaps 4;

Qy 42 AKAAQKQLOSEFGNEKTLQEQAKDILQTK---ADDLQAKSAMSNQAR----EDKQ 90
 Db 227 AQDVQEKLHQLEGRAFQMKQAEFLKAKISANDELRQKLVPENVGHLKONTEGHQ 286

Qy 91 REFLSLRRNPEEKSRDPARVEQENTURQYLQIAETIANKKGLKLVIDSASGSV 150
 Db 287 KSLLERSHLDQQVEFRLKVEPYGETENKALVQV---EDLFQKLG--PLAGDVEGHL 340

Qy 151 MYLKEQL 157
 Db 341 SFLERDL 347

RESULT 10
 US-09-198-452A-315
 ; Sequence 315, Application US/09198452A
 ; Patent No. 655924
 ; GENERAL INFORMATION:

```

; APPLICANT: Giffraais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198 452A
; SEQ ID NOS: 6849
; SEQ ID NO: 315
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1..158
; OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-315

Query Match Score 118; DB 4; Length 158;
Best Local Similarity 21.3%; Pred. No. 0.0047;
Matches 32; Conservative 43; Mismatches 69; Indels 6; Gaps 3;

Qy 27 IGVFNQSIAAMESAAAKAQKQLQS --EFGNEKTOLEQAKDQTKADDLQAKSAAMSN 83
Db 10 IGYVNLRKCLESIDLKKETBEAKQQFTVNAEKIEEETTSINRKLQD-EDIMNESLSD 68

Qy 84 QAREDKOREFELLRNFEKEKSRDFAIRVEQAENTLRLQYLAEEFIAKKGKLKLVL 143
Db 69 SASEELRKKFEDLSGFGYNAYOSQYTSINGNSVYKRIQEVKIAESTRSKERLEATL 128

Qy 144 DSAGSVMYLEKNUDJITKEILEANIAZAWKK 173
Db 129 NEE--AVLATAPGTOKTETIALLNESFKK 156

RESULT 11
US-08-714-741-32
; Sequence 32, Application US/08714741
; Patent No. 6500613
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks, Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
; TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
; TITLE OF INVENTION: PORTIONS AND PRODUCTS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Stafford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714-741
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Etienne, Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2460
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 32;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 991 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: amino acid
 US-08-714-741-32

Query Match 12.2%; Score 110; DB 4; Length 899;
 Best Local Similarity 24.3%; Pred. No. 0 6; Gaps 9;
 Matches 54; Conservative 36; Mismatches 72; Indels 60;

Qy	7 SMAILACILVANSAFASDFFPIGVENSQSSTAMESRAAKAQKKLOSEFGNEKTQLE-----	61
Db	1170 SVAIIGAGIVA-----SPTIVRAEFAAVASQSKAERDYDTAKRDAENAKKA 1216	
Qy	62 -KOAKDLOTKADDLQAK--SAAMSQNAREDKOPFELDRNFEKKSDF-----	107
Db	1217 LEEAKRQEKEYQDYQRRIEKEAKETQSLEQQ---BANKDYLKLKYLGRNLNSSS 1227	
Qy	108 --AIRVEAENTIROYALEQIVIAETI-----ARKKGURKVLVDASGSYML--	153
Db	1273 VLKKEMEEAEKKDKENQREFENKIRTEIVPNPQBLEMARRKS-EVKATESGLVTRVEEA 1331	
Qy	154 EKN-----LDITKELILEAINAWKGGSKLPEMANRKK 186	
Db	1332 ERNVTIDARQRQLVLIKNEVVLQAXXALESGGHKLEPKMNKK 1373	

RESULT 12
 US-08-006-676B-1
 Sequence 1, Application US/08006676B
 / Patient No. 5411865
 / GENERAL INFORMATION:
 / APPLICANT: Reed, Steven
 / TITLE OF INVENTION: Diagnosis of Leishmaniaisis
 / NUMBER OF SEQUENCES: 3
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Jeffrey B. Oster
 / STREET: 8339 SE 57th Street
 / CITY: Mercer Island
 / STATE: Washington
 / COUNTRY: USA
 / ZIP: 98040-4906
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC Comparable
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: WORD for Windows
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/006, 676B
 / FILING DATE: 15-JAN-1993
 / CLASSIFICATION: 435
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Oster, Jeffrey B.
 / REGISTRATION NUMBER: 32, 585
 / REFERENCE/DOCKET NUMBER: REED-4
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (206) 232-7845
 / TELEXFAX: (206) 236 0205
 / INFORMATION FOR SEQ ID NO: 1:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 955 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 US-08-006-676B-1

Query Match 12.1%; Score 108.5; DB 1;
 Best Local Similarity 26.5%; Pred. No. 0 043;
 US-08-006-676B-1

Matches 40; Conservative 32; Mismatches 52; Indels 27; Gaps 5; Db 877 Q----LESTAAKMSAEQDRESTRATE 900

Qy 35 TAMESEAKAAOKKQLOEFGNEKTQLEKQDQLQTADDLQK---SAAMSNQARED 89
Db 757 LASQLETAAKMSAEQDRENTATLEQQLDSEERAELASQLESTAARMSAEQDRES 816

Qy 90 QREFLELR-RNFEKSDFAIRV----QAEN----TIRQLAEQIYLAETIA 134
Db 817 TRATLEQQLDSEERAELASQLESTAARMSAEQDRESTRATEQQLDSEERAELAS 876

Qy 135 KKKGGLKLVLD9ASGSVNYLXKNLDITKEILE 165
Db 877 Q----LESTAAKMSAEQDRESTRATE 900

RESULT 13
US-08-282-845-2
Sequence 2, Application US/08282845
Patent No. 5719263

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: A 23kDa Antigen Present in Leishmania
NUMBER OF INVENTIONS: 3
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,414A
FILING DATE: 21 APR 1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Kadlecik, Ann T.
REGISTRATION NUMBER: 3,9,244
REFERENCE/DOCKET NUMBER: 210121-407
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723336 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 955 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-428-414A-3

Query Match Best Local Similarity 12.0%; Score 108.5; DB 2; Length 955;
Matches 40; Conservative 32; Mismatches 52; Indels 27; Gaps 5; Db 877 Q----LESTAAKMSAEQDRESTRATE 900

Qy 35 TAMESEAKAAOKKQLOEFGNEKTQLEKQDQLQTADDLQK---SAAMSNQARED 89
Db 757 LASQLETAAKMSAEQDRENTATLEQQLDSEERAELASQLESTAARMSAEQDRES 816

Qy 90 QREFLELR-RNFEKSDFAIRV----QAEN----TIRQLAEQIYLAETIA 134
Db 817 TRATLEQQLDSEERAELASQLESTAARMSAEQDRESTRATEQQLDSEERAELAS 876

Qy 135 KKKGGLKLVLD9ASGSVNYLXKNLDITKEILE 165
Db 877 Q----LESTAAKMSAEQDRESTRATE 900

RESULT 15
PCT-US94-00324-1
Sequence 1, Application PC/TUS94-00324
GENERAL INFORMATION:
APPLICANT: Reed, Steven
TITLE OF INVENTION: Diagnosis of Leishmaniasis
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington

COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word, version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00324
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/006,676
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 5004-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 955 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

Search completed: April 27, 2004, 09:38:11
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 27, 2004, 09:37:09 ; Search time 43 Seconds
(without alignments)
1195.916 Million cell updates/sec

Title: US-10-018-290a-1
Perfect score: 904
Sequence: 1 MKVKTSMAILACLLVANSA.....INAIAWKGGSKLPPEMANRKK 186

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
 1: /cn2_6/ptodata/2/pubpaas/us07_pubcomb.pep:
 2: /cn2_6/ptodata/2/pubpaas/us06_pub.pep:
 3: /cn2_6/ptodata/2/pubpaas/us06_new_pub.pep:
 4: /cn2_6/ptodata/2/pubpaas/us07_pct_new_pub.pep:
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 6: /cn2_6/ptodata/2/pubpaas/pctos_pubcomb.pep:
 7: /cn2_6/ptodata/2/pubpaas/us08_new_pub.pep:
 8: /cn2_6/ptodata/2/pubpaas/us08_pubcomb.pep:
 9: /cn2_6/ptodata/2/pubpaas/us09_pubcomb.pep:
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 11: /cn2_6/ptodata/2/pubpaas/us09c_pubcomb.pep:
 12: /cn2_6/ptodata/2/pubpaas/us09_new_pub.pep:
 13: /cn2_6/ptodata/2/pubpaas/us10_pubcomb.pep:
 14: /cn2_6/ptodata/2/pubpaas/us10c_pubcomb.pep:
 15: /cn2_6/ptodata/2/pubpaas/us10c_pubcomb.pep:
 16: /cn2_6/ptodata/2/pubpaas/us10_new_pub.pep:
 17: /cn2_6/ptodata/2/pubpaas/us10c_new_pub.pep:
 18: /cn2_6/ptodata/2/pubpaas/us10c_pubcomb.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-09-841-132-505
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatalia, Ajay.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.49C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO: 505
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae

US-09-841-132-505
Query Match 14.5%; Score 131; DB 9; Length 171;
Best Local Similarity 22.7%; Pred. No. 0 00081;
Matches 37; Conservative 44; Mismatches 76; Indels 6; Gaps 3;
Qy 14 LLVANSAFSADFPPIGVNSOIASMESEAAKAAQKKQS---EFGNEKTOLEKQAKDLQTK 70
Db 10 LLVNGSTSAAHANGYNNKRCBESDUGKETEAMKOQPKNAKKEELTSYNNK 69
Qy 71 ADDIQAQSAMSNQAREDKQREFELRNPFEEKSRDFAIRVEQVENTRQYLAEQIYLA 130
Db 70 LQD-EDYNELSDEASSEURKKFEDLSGRRYNAQSQQYTQSINQSVKRIQLICEVKTA 128
Qy 131 ETIARKKGKLRLVLLSAGSVMYLEKNLDITKETLEANAWK 173
Db 129 ESVSKERKEULAINNE--AVLAIAAPGTDKTEITAILNESFKK 169

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	131	14.5	171	9	US-09-841-132-505 Sequence 505, App
2	131	14.5	171	9	US-09-741-849-2 Sequence 2, Appl
3	131	14.5	171	15	US-10-312-273-77 Sequence 77, Appl
4	122	13.5	443	8	US-08-325-278-6 Sequence 6, Appl
5	118.5	13.1	382	9	US-09-800-729-206 Sequence 206, App
6	118.5	13.1	382	9	US-09-987-107-37 Sequence 37, Appl
7	111.8	13.1	158	15	US-10-289-762-115 Sequence 315, App
8	113.5	12.6	1130	15	US-10-369-493-5580 Sequence 510, App
9	113.5	12.6	1130	15	US-10-369-493-5581 Sequence 550, App
10	113.5	12.6	1190	15	US-10-369-493-5581 Sequence 1550, App
11	112.5	12.4	876	12	US-10-221-278-213 Sequence 273, App
12	112.5	12.4	876	15	US-10-291-172-273 Sequence 273, App
13	111.2	12.4	173	9	US-09-841-132-575 Sequence 573, App
14	112	12.4	1269	14	US-0-342-224-62 Sequence 62, Appl
15	109	12.1	2139	9	US-09-727-384-6 Sequence 6, Appl

RESULT 2
US-09-741-849-2
 i Sequence 2, Application US/097411849
 ; Patent No. US20020209918BA1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andrew D. MURDIN, Raymond P. COMEN, Joe WANG, Pamela DUNN
 ; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses thereof
 ; FILE REFERENCE: 7813-39
 ; CURRENT FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: US/09/741, 849
 ; PRIORITY FILING DATE: 1999-12-22
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 2
 ; LENGTH: 171
 ; TYPE: PRT
 ; ORGANISM: Chlamydia pneumoniae
 ; US-09-741-849-2

Query Match 14.5%; Score 131; DB 9; Length 171;
 Best Local Similarity 22.7%; Pred. No. 0.00081;
 Matches 37; Conservative 44; Mismatches 76; Indels 6; Gaps 3;

Qy 14 LIVVANSFAAAPSADPPIGVNSQSIAAMESAAKAKQQKLQS---BFGNEKTOLBKQAKOLQTK 70
 Db 10 LLVLGTSAAAHANGLYNLKRCLEESDIGKKETEELAMKOQVVAKEIEFELTSYNNK 69

Qy 71 ADDLQAKSAAMSNOAREDQREFLELRNFEKSRSRDAIRVEQAENTLROYLAEQIYLAA 130
 Db 70 LQP-EDYMESLSDASERLKRCKPEDLGSEYNAQSOYQSQNSVRIQLIQEVKIA 128

Qy 131 ETIAKKGLKLVLDLSASGSVMYLNKLDITKELEANAIAWAKK 173
 Db 129 ESYRSKEKLEATLINEE--AVLIAAPGTDKTTEIATLINESFKK 169

RESULT 3
US-10-312-273-77
 Sequence 77, Application US/10312273
 ; Publication No. US20040005667A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SPA
 ; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
 ; FILE REFERENCE: P205032WO
 ; CURRENT APPLICATION NUMBER: US/10/312, 273
 ; CURRENT FILING DATE: 2002-12-20
 ; PRIOR APPLICATION NUMBER: 0016363-4
 ; PRIOR FILING DATE: 2000-07-03
 ; PRIOR APPLICATION NUMBER: 0017047-2
 ; PRIOR FILING DATE: 2000-07-11
 ; PRIOR APPLICATION NUMBER: 0017983-8
 ; PRIOR FILING DATE: 2000-07-21
 ; PRIOR APPLICATION NUMBER: 0020440-4
 ; PRIOR FILING DATE: 2000-08-07
 ; PRIOR APPLICATION NUMBER: 0020440-4
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: 0027549-5
 ; PRIOR FILING DATE: 2000-11-10
 ; PRIOR APPLICATION NUMBER: 0031705-5
 ; PRIOR FILING DATE: 2000-12-22
 ; NUMBER OF SEQ ID NOS: 664
 ; SOFTWARE: SeqWin99, version 1.02
 ; SEQ ID NO: 77
 ; LENGTH: 171
 ; TYPE: PRT
 ; ORGANISM: Chlamydia pneumoniae
 ; US-10-312-273-77

Query Match 14.5%; Score 131; DB 15; Length 171;
 Best Local Similarity 22.7%; Pred. No. 0.00081;

Matches 37; Conservative 44; Mismatches 76; Indels 6; Gaps 3;

Qy 14 LIVVANSFAAAPSADPPIGVNSQSIAAMESAAKAKQQKLQS---BFGNEKTOLBKQAKOLQTK 70
 Db 10 LLVLGTSAAAHANGLYNLKRCLEESDIGKKETEELAMKOQVVAKEIEFELTSYNNK 69

Qy 71 ADDLQAKSAAMSNOAREDQREFLELRNFEKSRSRDAIRVEQAENTLROYLAEQIYLAA 130
 Db 70 LQP-EDYMESLSDASERLKRCKPEDLGSEYNAQSOYQSQNSVRIQLIQEVKIA 128

Qy 131 ETIAKKGLKLVLDLSASGSVMYLNKLDITKELEANAIAWAKK 173
 Db 129 ESYRSKEKLEATLINEE--AVLIAAPGTDKTTEIATLINESFKK 169

RESULT 4
US-08-325-278-6
 ; Sequence 6, Application US/08325278
 ; Publication No. US20030027283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bivack, Lars
 ; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SBED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/325,278
 ; FILING DATE: 26-OCT-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McMasters, David D.
 ; REGISTRATION NUMBER: 33,963
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 443 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-325-278-6

Query Match 13.5%; Score 122; DB 8; Length 443;
 Best Local Similarity 33.4%; Pred. No. 0.017;
 Matches 40; Conservative 12; Mismatches 55; Indels 12; Gaps 4;

Qy 48 KLOSERGENEKTLQBLQARDLQADLQAKSAMSNQAREDKQREFLELRNFEKSRDF 107
 Db 48 KRAEELEFKAKOALDEDKDLFTKLKELQDQYDIAKESTSDQR---LEKELEEKKEAL 103

Qy 108 AIRVEQAENTLROYLAEQIYLAAETIAKKGLKLVLDLSAS---GSVYMLKEKNLD-ITKE 162
 Db 104 ELAQDASRDYHRATA---LEKELEEKKEALDQASQDYNANVLEKELEITIRE 158

RESULT 5
US-09-800-729-06
 ; Sequence 206, Application US/098000729
 ; Patent No. US2002068319A1
 ; GENERAL INFORMATION:

```

; APPLICANT: Ni et al. 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/155,709
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 32 Human secreted proteins
; SEQ ID NOS: 6849
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 32 Human secreted proteins
; SEQ ID NOS: 6849
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO: 315
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE: 
; NAME/KEY: SITE
; LOCATION: 1..158
; OTHER INFORMATION: Xaa=unknown or other
; US-10-289-762-315

Query Match
Best Local Similarity 25.8%; Pred. No. 0.029;
Matches 34; Conservative 29; Mismatches 47; Indels 17; Gaps 4;

Qy 42 AKAAQKLQSERGNEKTOLEQAKDQLTK---ADLQAKSAMSNQAR-----EDKQ 90
Db 227 ADQVQENLNHQEGLAQMKKQAEERAKAISANADERQKLPVAVNQHKGNT EGLQ 286
Qy 91 RFLFELRNFEKSRAIRVEAQENTLROYLAEQYIYLAAETIAKKKGKLVYLDSSAGSV 150
Db 287 KSLLELRSHLDQVEEPRLKVEPYGEFENKALVQQ---EDLRQKLG--PLAGDVEGHL 340
Qy 151 MYLEKNI 157
Db 341 SFLEKDL 347

RESULT 6
US-09-987-107-37
; Sequence 37, Application US/09987107
; PATENT NO. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVESSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 37
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Sus scrofa
; US-09-987-107-37

Query Match
Best Local Similarity 26.8%; Pred. No. 0.029;
Matches 34; Conservative 29; Mismatches 47; Indels 17; Gaps 4;

Qy 42 AKAAQKLQSERGNEKTOLEQAKDQLTK---ADLQAKSAMSNQAR-----EDKQ 90
Db 227 ADQVQENLNHQEGLAQMKKQAEERAKAISANADERQKLPVAVNQHKGNT EGLQ 286
Qy 91 RFLFELRNFEKSRAIRVEAQENTLROYLAEQYIYLAAETIAKKKGKLVYLDSSAGSV 150
Db 287 KSLLELRSHLDQVEEPRLKVEPYGEFENKALVQQ---EDLRQKLG--PLAGDVEGHL 340
Qy 151 MYLEKNI 157

RESULT 7
US-10-289-762-315
; Sequence 35, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO: 315
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE: 
; NAME/KEY: SITE
; LOCATION: 1..158
; OTHER INFORMATION: Xaa=unknown or other
; US-10-289-762-315

Query Match
Best Local Similarity 21.3%; Pred. No. 0.01;
Matches 32; Conservative 43; Mismatches 69; Indels 6; Gaps 3;

Qy 27 IGVENSIAMSEAAKQKLSQ---EFGNEKTQLEQAKDLOTAKKDLOQAKSAMSN 83
Db 10 LGYVNLRCLLESDLGKETELEXQOFVNAEKFEELTSIYNKLQD-EDYMESLSD 68
Qy 84 QAREDKOREEFELRNFEKSRAIRVEAQENTLROYLAETIAKKKGKLVYL 143
Db 69 SASEBELRKFDLSEKQDNLDTKEILAINAMKK 173
Qy 144 DSASGSUIMYLEKNLDITKEILAINAMKK 173
Db 129 NEE--AVIAIAQTGDKTEILAINNESFKK 156

RESULT 8
US-10-369-493-5580
; Sequence 5580, Application US/10369493
; Publication No. US2003033367A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianteng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/3160,039
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO: 5580
; LENGTH: 1130
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-10-369-493-5580

Query Match
Best Local Similarity 23.9%; Pred. No. 0.31;
Matches 32; Conservative 34; Mismatches 45; Indels 23; Gaps 5;

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RESULT 9
US-10-369-493-5581
Sequence 5581, Application US/10369493
; GENERAL INFORMATION:
; Publication No. US20030233675A1
; APPLICANT: Cao, Yongwei
; Hinkle, Gregory J.
; Slater, Steven C.
; Goldman, Barry S.
; Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR APPLICATION NUMBER: US 60/360,039
PRIORITY FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 47374
LENGTH: 1130
TYPE: PRT
ORGANISM: *Caenorhabditis elegans*
US-10-369-493-5581

Query Match 12.6%; Score 113.5; DB 15; Length 1130;
Best Local Similarity 23.9%; Pred. No. 0.31; Mismatches 34; Indels 23; Gaps 5;
Matches 32; Conservative 34; Mismatches 45; Indels 45; Gaps 5;

Qy 38 ESEAAAKAQKQLOSEPNEKTIQLEKQAKDLOQAKSAMNSQAR--KOREFL 94
Db 283 KQEAQKILQDTKKEYAKNARATEVKIQTKEFDEVEQDAETIA-EAREDDAKKRKV 341

Qy 95 ELLRNFEKSRDFAIRVQEANTLROYLAQIYLAETIA-KKKGLKLVIDSAGSYMYLE 154
Db 342 E----FEKEK-----IRECQSIKTTSEKCYMERTIVNAEVRILLKEK-----Q 382

RESULT 10
US-10-369-493-18546
Sequence 18546, Application US/10369493
; GENERAL INFORMATION:
; Publication No. US20030233675A1
; APPLICANT: Cao, Yongwei
; Hinkle, Gregory J.
; Slater, Steven C.
; Goldman, Barry S.
; Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIORITY FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 47374
LENGTH: 1190
TYPE: PRT

Query Match 12.4%; Score 112.5; DB 12; Length 876;
Best Local Similarity 29.2%; Pred. No. 0.28; Mismatches 24; Indels 23; Gaps 6;
Matches 42; Conservative 24; Mismatches 55; Indels 23; Gaps 6;

Qy 35 IAMESEAAK--AKOKLQLOSEPNEKTIQLEKQAKDLOQAKSAMNSQAR--EDKQ 90
Db 144 VCLEGHQVKLNAAEMLQOEL-LSRTSLQTKDLMTVEBLKLKGMEKEQRQEERKQ 202

Qy 91 REFLEDRNFEEKSRDFAIRVQEANTLROYLAQIYLAETIA-KKKGLKLVIDSAGSYMYLE 137
Db 203 RKABEL---QELHLKIKYEELENERNQYEWKUKATKAEVQALQEQVALDKAETERLH 258

Qy 138 GLKVLDSASGSVMYLEKNDITK 161
Db 259 S-QLSRTRAHNSHTERD&IQR 281

! SOFTWARE: PatentIn version 3.0
! SEQ_ID NO 6
! LENGTH: 2139
! TYPE: PRT
! ORGANISM: Homo sapiens
US-09-727-384-6

Query Match Score 109; DB 9; Length 2139;
Best Local Similarity 24.0%; Pred. No. 1.8;
Matches 40; Conservative 37; Mismatches 66; Indels 24; Gaps 6;

QY 41 AAKAAQKQLQSSEFGNEKTLQERKQARDLQTAADDLQAKSAAMSN---QAREDQREFILE 95
DB 652 SCKKAQENMKQRHENNTTRLEKQISDLKNEAELQOAAVILKEAHATCRHEEKKQLQ 711

OY 96 L----RNPFEEKSR---DFAIRYQAENTLROYLAEQTYLAETIAKKKGKLVLDS 145
DB 712 VKLEEEKTHLQEKLRLQGHEMBLKARLTQAOASFERE-REGIQQSSAWTEEKVRLGTQLEQ 770

OY 146 ASGSVM-----YLERNLDITKETILEAINAAWKCGSKLPEMANR 185
DB 771 PHQEQLTSLIVEKHTLEK-ELRKELIEKHORELQESREKOMETECNR 816

Search completed: April 27, 2004, 09:42:55
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 27, 2004, 09:33:33 ; Search time 20 seconds

(without alignments)
894.581 Million cell updates/secTitle: US-10-018-290A-1
Perfect score: 904
Sequence: 1 MKVTKLMSMAILCLLYVANSA.....INAATKGGSKLPEMANRKK 186Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	186	20.6	165	2 AD0129	cationic 19 Kda outer membrane protein precursor ompH [imported] - Yersinia pestis (s
2	179.5	19.9	168	2 G83190	cationic 19 Kda outer membrane protein precursor - Haemophilus ducreyi
3	169	18.7	143	2 S19728	probable outer membrane protein - Haemophilus ducreyi
4	163	18.0	162	2 H70314	hypothetical protein - Haemophilus ducreyi
5	137.5	15.2	169	2 A82099	outer membrane protein - Haemophilus ducreyi
6	136.5	15.1	197	2 E64102	probable outer membrane protein - Haemophilus ducreyi
7	134.5	14.9	161	1 DNBC17	outer membrane protein - Haemophilus ducreyi
8	134.5	14.9	161	2 D90651	histone-like protein - Haemophilus ducreyi
9	134.5	14.9	161	2 D85502	hypothetical protein - Haemophilus ducreyi
10	134	14.8	166	2 F81228	probable outer membrane protein - Haemophilus ducreyi
11	133	14.7	166	2 E82000	outer membrane protein - Haemophilus ducreyi
12	131.5	14.5	161	1 S09104	probable outer membrane protein - Haemophilus ducreyi
13	131.5	14.5	161	2 AC0530	outer membrane protein - Haemophilus ducreyi
14	131	14.5	171	2 E72094	cationic outer membrane protein - Haemophilus ducreyi
15	131	14.5	171	2 E86528	ompH-like outer membrane protein precursor - Haemophilus ducreyi
16	128.5	14.2	484	2 S35401	M1 protein precursor - Haemophilus ducreyi
17	124.5	13.8	227	2 S01260	M1 protein precursor - Haemophilus ducreyi
18	124.5	13.8	484	2 S46489	M1 protein precursor - Haemophilus ducreyi
19	123.5	13.7	484	2 S34978	M1.1 protein precursor - Haemophilus ducreyi
20	116.5	12.9	697	2 T07111	MAR binding filimentous protein precursor - Haemophilus ducreyi
21	114.5	12.7	630	2 T38023	probable transcriptase - Haemophilus ducreyi
22	111.4	12.6	1298	2 T24480	hypothetical protein - Haemophilus ducreyi
23	113.5	12.6	1130	2 T20288	hypothetical protein - Haemophilus ducreyi
24	113.5	12.6	1190	2 E84193	chromosome segregation protein - Haemophilus ducreyi
25	112.5	12.4	1940	1 A24922	myosin heavy chain - Haemophilus ducreyi
26	111.2	12.4	173	2 C71539	probable (ompH)-like protein - Haemophilus ducreyi
27	111.5	12.3	279	2 D71453	hypothetical protein - Haemophilus ducreyi
28	111.5	12.3	173	2 A81694	cationic outer membrane protein precursor - Haemophilus ducreyi
29	111.5	12.3	389	2 A43715	

SUMMARIES

RESULT 1	Query Match	Best Local Similarity	Score	DB 2	Length	Matches	Conservative	Mismatches	Indels	Gaps
	QY	4	KTLMIAILCLIVANSAFASDADPFGVENSQSIAMESEAAKAQKLIQSEFGNEKTQLEKQ	63	30.7%	30	33	8.9e-06	7	2
	Db	3	KWLCAASLGGLAASASAVQADKLAIVNTSSIFQQLPARAVAKOLENEFKGRATELOGM	62						
	Qy	64	AKDLQTKAADDIQAQSAAAMSNOQAEDQKREPEFLERLNFEEKSRDFA-IRVEAQANTLRQY	121						
	Db	63	ERDLQTKMQKLQRDSTMKA8DRTKELEMNMKQRETESTKAQF5QDNRRRAEE-RNK	120						
	Qy	122	LAEQTYLAETTAETKKGKGLVLVDASGSWMYLEKNLDITKEILEI	167						
	Db	121	ILSRQDADSVATRKGVDVII--ANAVAYADSSKDITADVILKV	164						

RESULT 2

G83190

probable outer membrane protein precursor PA3647 [imported] - *Pseudomonas aeruginosa*

C;Species: *Pseudomonas aeruginosa*

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C;Accession: G83190

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Adamian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.

Nature 406, 952-964, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen

A;Reference Number: A82350; PMID:20437337; PMID:10984043

A;Accession: G83190

A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-168 <STO>
A;Cross-references: GB:AE004784; PIDN:ANG07035_1; GSDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA3647

Query Match 19.9%; Score 179.5; DB 2; Length 168;
Best Local Similarity 30.4%; Pred. No. 2, 5e-05;
Matches 52; Conservative 38; Mismatches 72; Indels 9; Gaps 4;

Qy 1 MKVKTLSMALLCLVANSAFSADFPFGVENSQIAMESEAAKAQQKLOQSRFG--NEK 57
Db 1 MRKFTQFVLTAAIMAAPSAP-AEMKAVLNQMLLSDAAKQAYDAEKKFGPQLNLK 59

Qy 58 TQELEKQAKDQLQKADDLQAKSAAMSNGAREDQREFELRNFEEKEERDFAIRVEQAENT 117
Db 60 KNDLERDALKQ--DKVNSGSKRMSQDREKAELDFKQARDQFQSKELNESKAADDR 116

Qy 118 LROYLAEQYLAETIAKKGKGLKLVLDASGSVMYLEKNLDITKEILBAIN 168
Db 117 MLKKLKPKLQDAVEETIKGGIDMWIE-RGAVVDPKPQXDITRQYTERMN 165

RESULT 3
S19728 outer membrane protein ompH - Yersinia pseudotuberculosis (fragment)
C;Species: Yersinia pseudotuberculosis
C;Date: 13-Jan-1995 #sequence_revision 22-May-1998 #text_change 17-Mar-1999
C;Accession: S19728
R;Vuorio, R.; Hirvas, L.; Raybourne, R.B.; Yu, D.T.Y.; Vaara, M.
'Biochim. Biophys. Acta' 119, 124-126, 1991
A;Title: The nucleotide and deduced amino acid sequence of the cationic 19 kDa outer membrane protein of Yersinia pseudotuberculosis. A comparison with the 19 kDa outer membrane protein of Yersinia enterocolitica. A;Reference number: S19728
A;Accession: S19728
A;Molecule type: DNA
A;Residues: 1-143 <VTO>
A;Cross-references: EMBL:M73247
C;Genetics:
A;Gene: ompH
C;Superfamily: DNA-binding 17K protein
C;Keywords: membrane protein

Query Match 18.7%; Score 169; DB 2; Length 143;
Best Local Similarity 30.8%; Pred. No. 0.0001; Indels 6; Gaps 3;

Matches 44; Conservative 30; Mismatches 63; Indels 6; Gaps 3;

Qy 27 IGVENNSQIAMESEAAKAQQKLOQSERGNEXTQLEKARDLQTADLQAKSAMSNQAR 86
Db 4 IAVINNSQIIFQQLPARAVAKQLENPEFKGRATEQGMERDLQTMQKLQDGSTMKASDR 63

Qy 87 EDKQRELRNFEEKSRDFEA--IRVEQAENTLRLQYAEQYLAETIAKKGKGLKLVLD 144
Db 64 TYKLEMNTMKQRSTETSTQAQFFQDNRRQAAE--RNKILSRIQDAVSKVATKGGYDDVVD 121

Qy 145 SASGSVMYLEKNLDITKEILEAI 167
Db 122 -ANAVAYADSSRDITADVLCQV 142

H70314 hypothetical protein agl157 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: H70314
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; PMID:9537320
A;Accession: H70314
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
A;Residues: 1-162 <QF>
A;Cross-references: GB:AE000676; PIDN:G2982884; PIDN:AAC06512_1; PIDN:G2982893; GB:AE001
A;Experimental source: strain VF5
C;Genetics:
A;Gene: agl157

Query Match 18.0%; Score 163; DB 2; Length 162;
Best Local Similarity 28.3%; Pred. No. 0.003; Mismatches 61; Indels 16; Gaps 4;

Matches 45; Conservative 37; Mismatches 61; Indels 16; Gaps 4;

Qy 15 LVANSAFSADPPIGVENSQIAMESEAAKAQQKLOQSERGNEXTQLEKARDLQTADL 74
Db 14 LIAGISFSLDF -ACVDTNKVIRESKPLAQATLREK-----LEYQKQLIEQKQKL 64

Qy 75 QA----KSAAMSNQAREDKOREFLLELRNPFEEKSRDFAIRVEQAENTLQYLAEOYLA 129
Db 65 EALKKSLESKALEXAKEXKEKAYAKELEDELRKQVBAQSKLSRKKAELKMFDRVKIKI 124

Qy 130 AETIARKKGKGLKLVLDASGSVMYLEKNLDITKEILEAIN 168
Db 125 VESTAKKKKIKAVFD-CNSMLWYDVKDITNEVILKELD 161

RESULT 5
S19729 outer membrane protein OmpH VC2251 [imported] - Vibrio cholerae (strain N16961 serogroup O1) #text_change 02-Feb-2001
C;Species: Vibrio cholerae
C;Accession: A82099
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. J.; Durkin, S.; Haft, D.; Hickey, E.; Karp, P.; Kelliher, A.; Kibbe, A.; Lai, Z.; Long, C.; Madupu, R.; Nelson, J.J.; Overbeek, R.; Plumb, R.; Richardson, D.; Ronning, S.; Salzberg, S.; Salzberg, S.; Qin, H.; Brinkac, L.M.; Sutton, G.; Utterback, A.R.; Venter, J.C.; Fraser, C.M.
A;Title: The nucleotide and deduced amino acid sequence of the cationic 19 kDa outer membrane protein of Vibrio cholerae. A;Reference number: S19729
A;Accession: S19729
A;Molecule type: DNA
A;Residues: 1-169 <HEI>
A;Cross-references: GB:AB004297; PIDN:99656810; PMID:20406833; PMID:10952301
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-169 <HEI>
A;Cross-references: GB:AB003852; PIDN:995395_1; GSDB:GN
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC2251
A;Map Position: 1
C;Superfamily: DNA-Binding 17K protein

Query Match 15.2%; Score 137.5; DB 2; Length 169;
Best Local Similarity 24.0%; Pred. No. 0.015; Mismatches 46; Indels 3; Gaps 2;

Matches 40; Conservative 39; Mismatches 46; Indels 3; Gaps 2;

Qy 1 MKVKTLSMALLCLVANSAFSADFPFGVENSQIAMESEAAKAQQKLOQSERGNEXTQLEKARDLQTADL 60
Db 5 IKAASGLLIUSSMMANAAQ-KIGYINTAQVFEQALPOREVQVQKQMBEFKQAAEL 63

Qy 61 EKQAKDQLQTADLQKSAAMSNOAREDQREFELRNRFEKSDFAIRVEQAENTLQ 120
Db 64 QAIQADAKTKEFLKEDQGLMGQDVEEKURIEGOLDSKYKIKAQALEQASARRAEAEKQ 123

Qy 121 YLABQYLAESTIAKKGKGLKLVLDASGSVMYLEKNLDITKEILEAI 167
Db 124 KLFKVIQDAVKVAEKEGYDIVLDPS-SMOYQKDPHNLSKEVKIKI 168

RESULT 6
E64102 ssp protein - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Accession: E64102
R;Pleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirnness, E.F.; Kerlavage ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.; Glodek, A.; Kelley, J.M.; Weidmar , D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.

RESULT 7						
DNNEC17						
	outer membrane protein hmpA precursor - Escherichia coli (strain K-12)					
N	Alternative names: DNA-binding 17K protein; histone-like protein hmp					
C	Species: Escherichia coli					
C	Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 01-Mar-2002					
	Accession: JF0304 ; A38063 ; S13728 ; B64742 ; 154944 ; S20426					
R	Holick, A. ; Klepe, K.					
G	Gene: 67 , 117-124, 1588					
A	Article: Cloning and sequencing of the gene for the DNA-binding 17K protein of Escherichia coli					
A	Reference number: JTC0304 ; M012 ; 8832975 ; PMID:2843433					
A	Molecule type: DNA					
A	Accession: JF0304					
A	Residues: 1-161 <D1C>					
A	Cross-references: GB:M21118 ; NID:9147821 ; PIDN:AAA24630_1 ; PMID:9147822					
A	Molecule type: protein					
A	Accession: 21-30 <R02>					
A	Experimental source: strain K-12					
R	Dicker, I.B. ; Seetharam, S.					
B	Science, 173, 334-341, 1991					
A	Title: Cloning and nucleotide sequence of the firA gene and the firB200 (T5) allele from					
A	Reference number: S13728 ; M012 ; 9100302 ; PMID:1987124					
A	Accession: S13728					
A	Status: preliminary					
A	Molecule type: DNA					
A	Accession: 72-161 <BLAT>					
A	Cross-references: GB:AE000127 ; GB:U00096 ; NID:91786370 ; PIDN:AACT3289_1 ; PMID:91786375 ;					
A	Experimental source: strain K-12, substrain MG155					
R	Blattner, F.R. ; Plunkett III, G. ; Bloch, C.A. ; Perna, N.T. ; Burland, V. ; Riley, M. ; Cole, R.J. ; Rosse, D.J. ; Maurer, B. ; Shao, Y.					
S	Science, 277, 1453-1462, 1997					
A	Title: The complete genome sequence of Escherichia coli K-12.					
A	Reference number: A64722 ; M012 ; 97426617 ; PMID:9278503					
A	Accession: B64722					
A	Status: nucleic acid sequence not shown; translation not shown					
A	Molecule type: DNA					
A	Accession: 1-161 <BLAT>					
A	Cross-references: GB:AE000127 ; GB:U00096 ; NID:91786370 ; PIDN:AACT3289_1 ; PMID:91786375 ;					

R:Hirvay, L.; Koski, P.; Vaara, M.	Qy	14	LIVVANSFASDFFIGVNSQQ	Query Match
J: Bacteriol. 173, 1223-1229, 1991	Db	12	LALATSAQD-KIAIYNGMG	C:Superfamily: DNA-binding 17K protein
A:Title: The ornB gene of Yersinia	Qy	74	IQAKSRAAMSQNAREDKOREFV	C:Keywords: membrane protein
A:Reference number: 1544944; MUID:9	Db	71	LQSMKAGSD--RTKLEKDV	F:1-20/Domain: signal sequence #st
A:Accession: 154944	Qy	134	AKKKGLKLVLDSASGSYMWLL	F:21-161/Product: outer membrane protein
A:Molecule type: DNA	Db	128	ANSQDIDLVVD--ANAVAYNN	C:Comment: The hlpA protein has been isolated from GB/EMBL/1
A:Residues: 1-14; L-16-148; E-154-159				C:Genetics:
A:Cross-references: EMBL:75465; NCBI				A:Gene: hlpA; skip
C:Comment: The hlpA protein has been isolated from GB/EMBL/1				C:Superfamily: DNA-binding 17K protein
				C:Keywords: membrane protein
				F:1-20/Domain: signal sequence #st
				F:21-161/Product: outer membrane protein
Query Match		14-9%		
Best Local Similarity		25-8%		
Matches		36		
40; Conservative				

D85502 hypothetical protein hlpA [imported] - *Escherichia coli* (strain O157:H7, substrate EDL99) C;Species: *Escherichia coli*
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: D85502
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glazner, J.D.; Rose, D.J.; Mayhew, J.; Miller, L.; Grothe, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamitis, K.; Apodaca, M.; Nature, 409, 529-533, 2001.
A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A;Reference: A85480; MUID:21074935; PMID:11206551
A;Accession: D85502
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-161 <STO>
A;Cross-references: GB:AE005174; NID:gi12512906; PIDN:AGC54480.1; GSPDB:GN00145; UWGP:2001
A;Experimental source: strain O157:H7, substrate EDL933
C;Genetics:
A;Gene: hlpA
C;Superfamily: DNA-binding 17K protein

	Query Match	Score	DB	Length
Qy	14 LIWANSAASDADFIGVENSQSIMMSEAAKAKQKQGSEFGNEKTEQKQNDLQPKADD	134.5	2	161
Db	12 LAIATSAQAAD-KIAIVNMGSLSFQVQAKTGVSYNTLENEFKGRASEFQRMETDLQAKMKK	25.8	23	72
Qy	74 LQRAKSAAAMSNOAREDQKFELLELRNNFEKRSDFAIARVEQAENTLRQYLAQYLLAETI	127	36	72
Db	71 LQSMKAGSD--RTKLEDDVMARQTFAQKAPEQDARRNSNEERGKLVTRITQAVKSV	13.3	40	72
Qy	134 AKRGKGLXLYLDSSAISGSMVYKLNLI-DITKEILFATI	167	36	72
Db	128 ANSODIDLVV--ANAVAYNSSSVKDITADVLRKV	1.0	36	72

RESULT 10

F81228 outer membrane protein OmpH, probable NMB0181 [imported] - *Neisseria meningitidis* (strains)
C;Species: *Neisseria meningitidis*
C;Accession: F81228
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
R;Pettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.J.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Qin, H.; Yamamoto, J.; Gill, J.; Scarlato, V.; Masiagnani, V.; Pizza, M.; Science 287, 1809-1815, 2000.
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.; Villani, P.; Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A;Reference number: AB11000; MUID:20175755; PMID:10710307
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-166 <TET>
A;Cross-references: GB:AE002375; GB:AE002098; NID:97225394; PIDN:AAF40638.1; PID:972254
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0181

	Query Match	Score	DB	Length
Qy	4 KTLSMAILACILVANSFAASFADPFIGVENSQSIAMESEAAKAQKLOSEFGNEKTEQK	124	2	166
Db	5 RAPALARIGLQCTTAGAHADTFQKIGFINTERIYLESQKARIQKORTLDSBEFSARQDELQR-	27.3	26	63
Qy	64 AKDQTKADDLQQA-S-----ANSQNAEEDKQR---EFLEERRNFNEKSKRPAIVEQ	11.3	48	63
Db	65 --LORQLGLERLQIAEGLKRNAAQAA-EKKGGLVAAFRKGQAOFEE--DYNLRNE	1.0	48	64
Qy	114 AENTRQYLAEQYIYIAAETTAKKGKLXVLDASGSVMYLEKNUDITKEILEINA	1.69	48	64

A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 98-161 <H12>
A;Cross-references: GB:M35193
C;Genetics:
A;Gene: ompH
A;Start codon: GTG
C;Superfamily: DNA-binding 17K protein
C;Keywords: membrane protein
P;1-20/Domain: signal sequence #status predicted <SIG>
P;21-161/Product: outer membrane protein ompH #status predicted <MAT>
Query Match 14.5%; Score 131.5; DB 1; Length 161;
Best Local Similarity 25.2%; Pred. No. 0.037;
Matches 39; Conservative 35; Mismatches 74; Indels 7; Gaps 4;
QY 14 LLVANSFAADFPIGVNSOASIAMEAAQKKLQSERFGEQNEKTQLEQAKDILQTKADD 73
DB 12 LAMTVAQAAD-KIAIVMGNLFQQVAQTKGVSNLNEFKGRAELQRMETDLSQMQR 70
QY 74 LOAKSAMSNQAREDQREFELRNRNFEKSRSRDFAIRVEAENTLROYLAEQIYLAETI 133
DB 71 LQSMKAGSD--RTKLEKDMQSQRQTAQAFKDRARRSNEERBNLVRTRQAVKRV 127

QY 134 AKKGGLKLVLDSASGSVMYLEKLN-L-DITKEILEAI 167
DB 128 ANDQSTDLYVD--ANTVAVNSSDVDTADYLKV 160

RESULT 13
AC0530 Outer membrane protein OmpH precursor [imported] - *Salmonella enterica* subsp. *enterica*
C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
A;Note: this species has also been called *Salmonella typhi*
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AC0530
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davies, R.M.; Dowd, L.; White, N.; Farrar, I.S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar
A;Accession number: AB0502; MUID:11677608
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-161 <DNA>
A;Cross-references: GB:AL513382; PIDN: CAD08683.1.; PMID:916501506; GSPDB:GN00176
C;Genetics:
A;Gene: ompH
C;Superfamily: DNA-binding 17K protein

Query Match 14.5%; Score 131.5; DB 2; Length 161;
Best Local Similarity 25.2%; Pred. No. 0.037;
Matches 39; Conservative 35; Mismatches 74; Indels 7; Gaps 4;
QY 14 LLVANSFAADFPIGVNSOASIAMEAAQKKLQSERFGEQNEKTQLEQAKDILQTKADD 73
DB 12 LAMTVAQAAD-KIAIVMGNLFQQVAQTKGVSNLNEFKGRAELQRMETDLSQMQR 70

QY 74 LOAKSAMSNQAREDQREFELRNRNFEKSRSRDFAIRVEAENTLROYLAEQIYLAETI 133
DB 71 LQSMKAGSD--RTKLEKDMQSQRQTAQAFKDRARRSNEERBNLVRTRQAVKRV 127

QY 134 AKKGGLKLVLDSASGSVMYLEKLN-L-DITKEILEAI 167
DB 128 ANDQSTDLYVD--ANTVAVNSSDVDTADYLKV 160

RESULT 14
E72094 Cationic outer membrane protein OmpH, probable CP0457 [imported] - *Chlamydophila pneumoniae*, *Chlamydophila pneumoniae*
C;Species: *Chlamydophila pneumoniae*, *Chlamydophila pneumoniae* (strain J138)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
A;Cross-references: E72094; DB:AB001615; GB:AE001363; PIDN:94376574; Pred. No. 0.042; Mismatches 44; Indels 6; Gaps 3;
A;Experimental source: strain CM0029
R;Read, T.D.; Brumham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McElratty, G.; Salzber Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of *Chlamydia trachomatis* MoPn and *Chlamydia pneumoniae* AR39
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: E72094
A;Molecule type: DNA
A;Residues: 1-171 <ARN>
A;Cross-references: GB:AB001615; PIDN:94376574; Pred. No. 0.042; Mismatches 44; Indels 6; Gaps 3;
A;Experimental source: strain CM0029
R;Read, T.D.; Brumham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McElratty, G.; Salzber Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of *Chlamydia trachomatis* MoPn and *Chlamydia pneumoniae* AR39
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: D81574
A;Molecule type: DNA
A;Residues: 1-171 <REA>
A;Cross-references: GB:AE002207; Pred. No. 0.042; Mismatches 44; Indels 6; Gaps 3;
A;Experimental source: strain AR39; HL cells
C;Genetics:
A;Gene: CP0457
A;Accession: CP0301; CP0457

Query Match 14.5%; Score 131; DB 2; Length 171;
Best Local Similarity 22.7%; Pred. No. 0.042; Mismatches 44; Indels 6; Gaps 3;
Matches 37; Conservative 44; Mismatches 76; Indels 6; Gaps 3;

QY 14 LLVANSFAADFPIGVNSOASIAMEAAQKKLQSERFGEQNEKTQLEQAKDILQTK 70
DB 10 LLVNGSTSAAAHANGGYNLKRCLEESDLGKKETEELANKQQFTVNAEKIEELTSINK 69

QY 71 ADDIQAQSAAMSNOAREDQREFELRNRNFEKSRSRDFAIRVEAENTLROYLAEQIYLA 130
DB 70 LQD-EDYMESLSDSASEEIRKFFDLSGEYNAXOSQYYOSINQNVRKIQLIEVKIAA 128

QY 131 ETIakkglklvlldsasgsymyleknldtkeileinaawkk 173
DB 129 ESVSKESKEKLEATIME--AVIATAPGTDKTTETTAIIINESFKK 169

A;Accession: A86491; MUID:20330349; PMID:10871362
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-171 <DNA>
A;Cross-references: GB:BA000008; PIDN:98978675; Pred. No. 0.042; Mismatches 44; Indels 6; Gaps 3;
A;Experimental source: strain J138
C;Genetics:
A;Gene: CP0301

Query Match 14.5%; Score 131; DB 2; Length 171;
Best Local Similarity 22.7%; Pred. No. 0.042; Mismatches 44; Indels 6; Gaps 3;

QY 14 LLVANSFAADFPIGVNSOASIAMEAAQKKLQSERFGEQNEKTQLEQAKDILQTK 70
DB 10 LLVNGSTSAAAHANGGYNLKRCLEESDLGKKETEELANKQQFTVNAEKIEELTSINK 69

QY 71 ADDIQAQSAAMSNOAREDQREFELRNRNFEKSRSRDFAIRVEAENTLROYLAEQIYLA 130
DB 70 LQD-EDYMESLSDSASEEIRKFFDLSGEYNAXOSQYYOSINQNVRKIQLIEVKIAA 128

QY 131 ETIakkglklvlldsasgsymyleknldtkeileinaawkk 173

Search completed: April 27, 2004, 09:37:36
Job time : 21 secs

Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5				
Searched:	141681 seqs, 52070155 residues					
Total number of hits satisfying chosen parameters:	141681					
Minimum DB seq length:	0					
Maximum DB seq length:	2000000000					
Post-processing:	Minimum Match 0% Maximum Match 100%					
Database :	SwissProt_42;*					
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
		SUMMARIES				
Result No.	Score	Query	Match	Length	DB ID	Description
1	186	20.6	165	1	OMPH_YERPE	P58607 <i>yersinia</i> pe
2	179.5	19.9	168	1	OMPH_PSEAE	Q9Hxy5 <i>pseudomonas</i>
3	169	18.7	143	1	OMPH_YERPS	P31520 <i>yersinia</i> ps
4	163	18.0	162	1	Y157_AQUAE	Q6547 <i>aquifex</i> aeo
5	158.5	17.5	164	1	OMPH_YERAE	P31519 <i>yersinia</i> en
6	137.5	15.2	169	1	OMPH_VIBCH	Q9Jkw1 <i>vibrio</i> chol
7	136.5	15.1	197	1	OM26_HAEIN	Q57783 <i>haemophilus</i>
8	134.5	14.9	161	1	HLPA_ECOLI	P11437 <i>escherichia</i>
9	131.5	14.5	161	1	OMPH_SALTY	P16974 <i>salmonella</i>
10	131	14.5	171	1	OMPH_CHLPN	Q9z6n7 <i>chlamydia</i> p
11	118.5	13.1	382	1	APA4_BIG	Q46109 <i>bus</i> <i>scrofa</i>
12	116.5	12.9	697	1	MFP1_LYCES	P92023 <i>lycopersico</i>
13	112.5	12.4	1940	1	MYH3_RAT	P12847 <i>rattus</i> norv
14	111.2	12.4	173	1	OMPH_CHLTR	Q9zn38 <i>chlamydia</i> t
15	111.5	12.3	173	1	OMPH_CHLMU	Q9pbt2 <i>chlamydia</i> m
16	111.5	12.3	389	1	M49_STRPY	P16947 <i>streptococcus</i>
17	109	12.1	193	1	OM25_PASMU	Q51922 <i>pasturella</i>
18	108.5	12.0	955	1	KINL_LEICH	P46865 <i>leishmania</i>
19	108.5	12.0	1976	1	MYHA_RAT	Q9j1t0 <i>rattus</i> norv
20	108	11.9	1191	1	SMC2_MOUSE	Q8cgq8 <i>mus</i> <i>musculus</i>
21	107	11.8	1962	1	MYSA_DROME	P05661 <i>drosophila</i>
22	107	11.8	4473	1	PLE1_CRIGR	Q9j155 <i>cricetulus</i>
23	106.5	11.8	283	1	TPMM_LOCMI	P31816 <i>locusta</i> mig
24	106.5	11.8	1790	1	USO1 YEAST	P25386 <i>saccharomyces</i>
25	106.5	11.8	1969	1	MSA_CAEEL	P12844 <i>caenorhabditis</i>
26	106.5	11.8	1976	1	MYHA_BOVIN	Q27991 <i>bos</i> <i>taurus</i>
27	105	11.6	722	1	MFPI_TOBAC	Q9m744 <i>nicotiana</i> t
28	105	11.6	790	1	EEA1_MOUSE	Q8bj66 <i>mus</i> <i>musculus</i>
29	105	11.6	1938	1	MS_AEQIR	P24733 <i>equiperfector</i>
30	104.5	11.6	1940	1	MYH3_HUMAN	P10155 <i>homo</i> <i>sapiens</i>
31	104	11.5	407	1	M21_STRPY	P50468 <i>streptococcus</i>
32	104	11.5	1203	1	SMC2_XENLA	P50513 <i>xenopus</i> lae
33	104	11.5	1947	1	MYSC_CAEEL	P12845 <i>caenorhabditis</i>

SQ	SEQUENCE	165 AA;	18279 MW;	982D3BEF3A66FBCC	CRC64;	Qy	58 TQEKOAKDLOTKADDOAKSAAMSNOAREDQREFLELRNFEKEKSRDFAIRVEQAENT 117	Db	60 RNLERDAKALQ -- DFLVNSGSKMSGDREAEELPKQRADFQSKEINESSRAADRD 116
Query Match	20.5%; Score 186; DB 1; Length 165;	Best Local Similarity 30.7%; Pred. No. 9.7e-06;	Mismatches 33; Indels 6; Gaps 3;			Qy	60 RNLERDAKALQ -- DFLVNSGSKMSGDREAEELPKQRADFQSKEINESSRAADRD 116	Db	118 LRQYLAEOIYLAETIAKKGLKLVDLSASGSVMSYLEKNDLTITKEILEAN 168
Best Local Similarity 30.5%; Matches 51; Conservative 33; Mismatches 76; Indels 6; Gaps 3;						Qy	118 LRQYLAEOIYLAETIAKKGLKLVDLSASGSVMSYLEKNDLTITKEILEAN 168	Db	117 MLKGKLPKLDQDAVEETIKGGYDVT--RGAVIDVKPQTDITRQIERN 165
Qy	4 KTLSMATAACLLVANSASFADPIGVENSQSTAMESPAKAQKLUOSEFGNEKTOLEKQ 63					RESULT 3			
Db	3 KWLCAAISGLALAASAYAQAAKDIATVNVSSFEQLPAREAVAKQLINEFKGRATELQGM 62					OMPH_YERPS			
Qy	64 AKDLQTADDLOAKSAMSNQAREDKOREFELLRNFEKEKSRDFA--IRVEQAENTLRQY 121					ID_OMPH_YERPS			
Db	63 ERDLQTMQKLQDGSIMKASDRTKLENEVMQREFESTKAQAFEQDNRRQAAE--RNK 120					STANDARD			
Qy	122 LABOIVLAETIAKKGLKLVDLSASGSVMSYLEKNUIDTKEILEAI 167					PRT;	143 AA.		
Db	121 ILSRIOQDAVKSVATKGGTDDVVTD--ANAVAYADSSSKDITADVLKQV 164								
RESULT 2									
OMPH_PSEAE									
ID	OMPHESEAE								
AC	Q9HX15;								
DT	28-FEB-2003	(Rel. 41, Created)							
DT	28-FEB-2003	(Rel. 41, Last sequence update)							
DT	28-FEB-2003	(Rel. 41, Last annotation update)							
DB	OmpB-like precursor.								
GN	OMPH								
OS	Pseudomonas aeruginosa								
CC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;								
CC	Pseudomonadaceae; Pseudomonas.								
CC	NCBI_TAXID=287;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN_NA								
RC	STRAIN_ATCC_15632 / PAO1;								
RC	MEDLINE=20437331; PubMed=10984043;								
RA	Stover C.K., Pham X.-Q.T., Erwin A.U., Mizoguchi S.D., Warrener P.,								
RA	Hickey M.J., Birrman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,								
RA	Garber R.L., Goletti L., Tolentino E., Westbrook-Wadman S., Yuan Y.,								
RA	Brody L.I., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,								
RA	Smith K.A., Spencer D.H., Wong G.-K.-S., Wu Z., Paulsen I.T.,								
RA	Reizer J., Sauer M.H., Hancock R.E.W., Lory S., Olson M.V.,								
RA	"Complete genome sequence of Pseudomonas aeruginosa PAO1, an								
RA	opportunistic pathogen."								
RA	Nature 406:1959-1964 (2000).								
CC	-!- SUBCELLULAR LOCATION: Outer membrane (Potential).								
CC	-!- SIMILARITY: BELONGS TO THE OMPH/HLP FAMILY.								
CC									
CC	Query Match								
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).								
CC									
DR	RP04784; AAC07035.1; -.								
DR	GB3190; GB190.								
DR	Interpro; IPR005632; OmpH.								
DR	Pfam; PF03938; OmpH; 1.								
KW	Outer membrane; Signal; complete proteome.								
FT	SIGNAL								
FT	CHAIN								
SQ	SEQUENCE 168 AA; 19090 MW; EEF0754C98740D96 CRC64;								
Qy	1 MKVKTLSMALLVANSASFADPIGVENSQSTAMESPAKAQKLUOSEFGNEKTOLEKQ 63								
Db	1 MRKFTQFLITAIAMAPSAPAF-AEMKTAVINQOMALIDESAAKQAYDAEKFGPQNLK 59								
Qy	1 MKVKTLSMALLVANSASFADPIGVENSQSTAMESPAKAQKLUOSEFGNEKTOLEKQ 63								
Db	1 MRKFTQFLITAIAMAPSAPAF-AEMKTAVINQOMALIDESAAKQAYDAEKFGPQNLK 59								
RESULT 4									
Y15_AQUAE									
ID	Y15_AQUAE								
AC	066547;								
DT	16-OCT-2001 (Rel. 40, Created)								

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Hypothetical protein AQ_157 precursor.
 GN AQ_157.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
 RN [1]
 SEQUENCE FROM N.A.
 STRAIN=VF5;
 MEDLINE=9819666; PubMed=9537320;
 Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
 Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 "The complete genome of the hyperthermophilic bacterium Aquifex
 aeolicus";
 RY Nature 392:353-358(1998).
 CC -!- SIMILARITY: BELONGS TO THE OMPH/HLPA FAMILY.

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DR EMBL; AE000676; AAC06512.1; -.
 DR PIR; H0314; H70314.
 DR InterPro; IPR00562; OmpH.
 DR Pfam; PF03938; OmpH; 1.
 KW Hypothetical protein; Coiled coil; Signal; Complete proteome.
 FT SIGNAL 1 21 POTENTIAL.
 FT DOMAIN 22 162 HYPOTHETICAL PROTEIN AQ_157.
 SQ SEQUENCE 162 AA; 18878 MW; 61DB961E197416 CRC64; COILED COIL (POTENTIAL);

Query Match 18.0%; Score 161; DB 1; Length 162;
 Best Local Similarity 28.3%; Pred. No. 0.00029;
 Matches 45; Conservative 37; Mismatches 61; Indels 16; Gaps 4;

Qy 15 IVVANSFAADFPPGIVFNSQIAMESEAKAAQKRLQSFGNEKTLQEXQAKDLQLQTADDL 74
 Db 14 LIAGISFSLDF--ACVDTMKVIRESKFLAKAQTELREK-----LETYQKLIEQKQL 64

Qy 75 QA----RGAAMENQAREDQREFLEIERNFEKSFRDAIRVEQAENTLROQLAEQYIA 129
 Db 65 BALKKSLSKALSEKAREKKAKEIQLDELRLKLOVEAQSUSRKRAELRNFVDKVTIKI 124

Qy 130 AETIARKKGKGLKVLDSASGSVMMYLEKNDITKSTILEAN 168
 Db 125 VESTAKRKRIKAVD--CNSMLYWDICKDITNEVNLKEED 161

RESULT 5
 OMPH_YEREN STANDARD; PRT; 164 AA.
 AC P31519
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cationic 19 kDa outer membrane protein precursor.
 GN OMPH.
 OC Yersinia enterocoliticia.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 RN [1]

SEQUENCE FROM N.A.
 MEDLINE=91123198; PubMed=1191717;
 RA Hirvas L., Koski P., Vaara M.;
 RT "The OmpH gene of Yersinia enterocolitica: cloning, sequencing,
 expression, and comparison with known enterobacterial OmpH

RT sequences.";
 RL J. Bacteriol. 173:1223-1229(1991).
 CC -!- SUBCELLULAR LOCATION: Outer membrane.
 CC -!- SIMILARITY: BELONGS TO THE OMPH/HLPA FAMILY.
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 CC -- M34854; AAA77658.1; -.
 DR InterPro; IPR005632; OmpH.
 DR Pfam; PF03938; OmpH; 1.
 KW Outer membrane; Signal; PRT; 164 AA; 18225 MW; 70F6C0B5B3C95B7B CRC64; CATIONIC 19 kDa OUTER MEMBRANE PROTEIN.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 164 AA; 18225 MW; 70F6C0B5B3C95B7B CRC64;
 SQ SEQUENCE 164 AA; 18225 MW; 70F6C0B5B3C95B7B CRC64;
 Query Match 17.5%; Score 158.5; DB 1; Length 164;
 Best Local Similarity 26.2%; Pred. No. 0.00057;
 Matches 43; Conservative 36; Mismatches 82; Indels 3; Gaps 2;
 Qy 4 KTLSMAILCLLYVANSFAADFPPGIVFNSQIAMESEAKAAQKRLQSFGNEKTLQEKQ 63
 Db 3 KWLAAASGLLALARASYOA-AKAIAVNVSRSFQQLPSETVAKRLEKQFGRATELOQM 61
 Qy 64 AKDILQTKADDLQAKSAMNSNQAREDQREFLEIERNFEKSFRDAIRVEQAENTLROYIA 123
 Db 62 ESDDQTRMQLQRLQDGSTMKAESDTKLENDVMKORETSTKAQEFQDNRRROMERNCL 121
 Qy 124 EQIYLAETIARKKGKGLKVLDSASGSVMMYLEKNDITKSTILEAN 167
 Db 122 SRIQDAVSKVASKGQDYVVID--ANAVAYADPSKDTADVLRKV 163
 RESULT 6
 OMPH_VIBCH STANDARD; PRT; 169 AA.
 ID OMPH_VIBCH
 AC OSPFWL
 AC OSPFWL
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Outer membrane protein ompH precursor.
 GN OMPH OR VC251.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 RN [1] NCBI TaxID=666;
 RN SEQUENCE FROM N.A.
 RC SPRAIN=1; TOR_N16961 / Serotype O1;
 RX MEDLINE=2046833; PubMed=10952101;
 RA Heidelberg J.P., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Embelava M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae.";
 RT Nature 406:47-48 (2000).
 CC -!- SUBCELLULAR LOCATION: Outer membrane (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE OMPH/HLPA FAMILY.
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CC EMBL; AB004297; AAF95395.1; -.

CC DR PIR; AB2099; AB2099.

CC DR TIGR; VC2251; -.

CC DR InterPro; IPR005632; OmpH.

CC DR Pfam; PF03936; OmpH; 1.

CC KW Outer membrane; Signal; Complete Proteome.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 169 OUTER MEMBRANE PROTEIN OMPH.

SQ SEQUENCE 169 AA; 18952 MW; 9G78ABCE21CC7 CRC64;

Query Match 15.2%; Score 137.5; DB 1; Length 169;

Best Local Similarity 24.0%; Pred. No. 0.013;

Matches 40; Conservative 46; Mi smatches 78; Indels 3; Gaps 2;

Qy 1 MKVKTISMAILACLVANSAFSADPPIGVNSQSAMESAAKAAQKLOQSEFGNKTKQL 60

Db 5 IKAASGLITLSSMANAAEAAQ-KIGVINTAQVFQALPQEAEVLQRQEEFKKAEL 63

Qy 61 BKKQAKDLOTKADDLOAKSAMNSNQREDKOREFLERLNREBEKSDFAIRVEQAHTNLQ 120

Db 64 QATQDADKTIKEKLRDGGLMQUEVEKRIEGGSKIKAGALEQASARPAEEHQ 123

Qy 121 YLAQFQYIYLAAETIAKKKGKLKVLDASGSYMLEVNLDITKELEAI 167

Db 124 KLFKVYQDAVKVQAEKEGYDIVDTS--SMQYGKEPHNLSEKVKAI 168

RESULT 7

OM26_HAETN STANDARD; PRT; 197 AA.

ID OM26_HAETN STANDARD; PRT; 197 AA.

AC Q9S693; Q9S691; Q9S692; Q9S699;

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Outer membrane protein 26 precursor.

GN OMP26 OR SKP 6 OR H0916.

OS Haemophilus influenzae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

OC Pasteurellaceae; Haemophilus.

OX NCBI_TAXID=27;

RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-Rd / KW20 / ATCC 51907;
RX SEQID=95353600; PubMed=7542800;

RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirrness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitchburg W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Heidelberg B., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Sudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann N.S.M., Graham C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C., "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.", Science 269:496-512 (1995).
RT [2]

RN SEQUENCE OF 24-30.

RP MEDLINE:20137488; PubMed=10675023;

RC STRAIN-NTH1; AND CHARACTERIZATION.

RC MEDLINE:99185023; PubMed=10085039;

RA El-Adhami W., Kyd J.M., Bastin D.A., Cripps A.W.; "characterization of the gene encoding a 26-kilodalton protein (OMP26) from nontypeable Haemophilus influenzae and immune responses to the recombinant protein.", Infect. Immun. 67:1935-1942 (1999).

RL [3]

RP SEQUENCE OF 24-30.

RC Langen H., Foutsas B., Evers S., Berndt P., Lahm H.W., Wipf B., Gray C., Fountoulakis M.;

- RX RA MEDLINE=88329735; PubMed=2843433;
 RA Holck A., Kleppe K.;
 RT "Cloning and sequencing of the gene for the DNA-binding 17K protein
 of *Escherichia coli*";
 RL Gene 6:117-124 (1988);
 RN [2]
 SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 Gregor J., Davies N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1433-1474 (1997).
 RN SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12 / W3110;
 RA Takedo K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T.,
 Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihara S.,
 Mizuno T., Makino K., Nakata A., Yura T., Sampai G., Mizobuchi K.,
 RT "Syntematic sequencing of the *Escherichia coli* genome: analysis of the
 PT 4.0 - 6.0 min (189,987 - 281,416 bp) region.";
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12 / ATCC 700930 / Serotype 2a;
 RX MEDLINE=21590274; PubMed=12704152;
 RA Blattner F.R., Plunkett G. III, Rose D.J., Darling A.,
 Fournier G., Mayhew G.F., Burland V., Venkatesan M.M., Deng W.,
 Wei J., Goldberg M.B., Plunkett G. III, Rose D.J., Darling A.,
 RA Hirvonen L., Coleman J., Koski P., Vaara M.;
 RA Mau B., Perna N.T., Payne S.M., Runyen-Jacobsen L.J., Zhou S.,
 Schwartz D.C., Blattner F.R.;
 RT "Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity
 RT through comparison with genomes of *Escherichia coli* K12 and O157.";
 RL Nucleic Acids Res. 30:4432-4441 (2002).
 RN [4]
 SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=2457T / ATCC 700930 / Serotype 2a;
 RX MEDLINE=21590274; PubMed=12704152;
 RA Blattner F.R., Plunkett G. III, Rose D.J., Darling A.,
 Fournier G., Mayhew G.F., Burland V., Venkatesan M.M., Deng W.,
 Wei J., Goldberg M.B., Plunkett G. III, Rose D.J., Darling A.,
 RA Hirvonen L., Coleman J., Koski P., Vaara M.;
 RA Mau B., Perna N.T., Payne S.M., Runyen-Jacobsen L.J., Zhou S.,
 Schwartz D.C., Blattner F.R.;
 RT "Complete genome sequence and comparative genomics of *Shigella*
 RT *flexneri* serotype 2a strain 2457T.";
 RL Infect. Immun. 71:2775-2786 (2003).
 RN [5]
 SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=S.TYPHIMURIUM OMPH.
 RX MEDLINE=22388234; PubMed=12471157;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 Rasio D., Buckles B.L., Liu S.-P., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.P., Rose D.J., Zhou S., Schwartzenbach D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaicism structure revealed by the complete genome sequence
 RT of uropathogenic *Escherichia coli*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
 RN [6]
 SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=O157:H7 / ATCC 700927;
 RX MEDLINE=2107935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamitis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7.";
 RL Nature 409:529-533 (2001).
 RN [7]
 SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 Han C.-G., Onitsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
 Kubara S., Shiba T., Hattori M., Shinagawa H.;
 RA "Complete genome sequence of enterohaemorrhagic *Escherichia coli*
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22 (2001).
 RN [8]
 SEQUENCE OF 72-161 FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;
 RX MEDLINE=1100302; PubMed=198124;
 RA Dicker I.B., Seetharam S.R.;
 RT "Cloning and nucleotide sequence of the *firA* gene and the *firA200*(Ts)
 allele from *Escherichia coli*.";

SQ	SEQUENCE	161 AA;	17688 MW;	2A968BBD83F3E675 CRC64;	
	Query Match	14.9%;	Score 134.5;	DB 1;	Length 161;
	Best Local Similarity	25.8%;	Pred. No. 0.02;		
	Matches 40;	Conservative	36; Mismatches	72;	Indels 7; Gaps 4;
QY	14	LLVANSFAFSADPEPIGVNSQSIAAMESAAKAQKLUQSEFGNEKTLQLEQAKDILQTKADD 73			
DB	12	LALATQAQAD-KIAVNMGSLFEQVAKTGSVNTLNEPKGRASSLQLQRMETDLQAMKK 70			
QY	74	LOQKSAMSNOAREDKOREFLERLNRRNEKSRSRDAIREQAEINTLROYLAEQIYLAETI 133			
DB	71	LQSMRAGSD--RTKLEKDVMARQTAFAQKQAFEDARRSNEERGKLVTRIQAVSKV 127			
QY	134	ARKKGKIKLVLDASGSVYMLEKKNL-DITKELEAI 167			
DB	128	ANSQDIDLVVDD--ANAVAYNSSDVKDITADVLKQV 160			
RESULT 9					
ID	OMP8 SALTY STANDARD:	PRT:	161 AA.		
AC	P16974;				
DT	01-AUG-1990 (Rel. 15, Created)				
DT	01-AUG-1990 (Rel. 15, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DB	Outer membrane protein omp precursor (Cationic 16 kDa outer membrane protein)				
DE	OMP8 OR SPM0225 OR STY0248 OR T0226				
GN	Salmonella typhimurium, and				
OS	Salmonella typhi.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				
OC	Enterobacteriaceae; Salmonella.				
OX	NCBI_TaxID=602, 601;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 21-30.				
RC	SPECIES=S:typhimurium;				
RC	MEDLINE=900370202; PubMed=2681205;				
RA	Rheen M., Kantele J., Vaara M.;				
RA	Koski P., Rheein M., Kantele J., Vaara M.;				
RA	"Isolation, cloning, and primary structure of a cationic 16-kDa outer membrane protein of <i>Salmonella typhimurium</i> ." ;				
RA	J. Biol. Chem. 264:18973-18981(1989).				
RN	SEQUENCE FROM N.A.				
RC	SPECIES=S:typhimurium;				
RC	MEDLINE=90255961; PubMed=187745;				
RA	Kirves L.-, Vaara M.;				
RA	"Complete sequence of the ompH gene encoding the 16-kDa cationic outer membrane protein of <i>Salmonella typhimurium</i> ." ;				
RA	Gene 88:117-120(1990).				
RN	SEQUENCE FROM N.A.				
RC	SPECIES=S:typhimurium; STRAIN=L72 / ATCC 700720;				
RA	Medline=21534948; PubMed=11677608;				
RA	Parkhill J., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Churcher C., Sanders K.E., Gwilliam R., Quail M.A., Price N.R., Thomson N.R., Pickard D., Wain J., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hantlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moulie S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,				
RA	"Comparative genomics of <i>Salmonella enterica</i> serovar Typhi strains Ty2 and CT18."				
RN	Nature 413:852-856 (2001).				
RA	Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant <i>Salmonella</i> enterica serovar Typhi CT18."				
RN	Nature 413:848-852 (2001).				
[5]					
RP	SEQUENCE FROM N.A.				
RC	SPECIES=S:typhi; STRAIN=Ty2 / ATCC 700931;				
RC	MEDLINE=22531367; PubMed=1264504;				
RA	Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;				
RA	"Comparative genomics of <i>Salmonella enterica</i> serovar Typhi strains Ty2 and CT18."				
RL	Bacteriol. 185:2330-2337 (2003).				
RN					
RP	SIMILARITY TO E.COLI_HPIA.				
RX	MEDLINE=90221355; PubMed=2313304;				
HRV	Hirvas L., Coleman J., Koski P., Vaara M.;				
RT	"Bacterial histone-like protein I, (Hlp-I) is an outer membrane constituent?"				
RT	FEBS Lett. 262:123-126 (1990).				
CC	-1 SUBCELLULAR LOCATION: Outer membrane.				
CC	-1 SIMILARITY: BELONGS TO THE OMP/ELP/FA FAMILY.				
CC					
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CC					
DR	EMLBL; J05101; AAA2170_1; -.				
DR	EMBL; AE008705; AAU119189_1; -.				
DR	EMBL; AL672266; CAD008683_1; -.				
DR	EMBL; AB016834; AAU07956_1; -.				
DR	PTIR; JQ0528; S09104.				
DR	StyGene; SG10265; omph.				
DR	InterPro; IPR005632; omph.				
DR	Pfam; PF03938; Omph_1.				
DR	Outer membrane; Signal; Complete proteome.				
KW	Outer membrane; Signal; Complete proteome.				
FT	SIGNAL 1 20				
FT	CHAIN 21 161 OUTER MEMBRANE PROTEIN OMPH.				
SQ	SEQUENCE 161 AA; CF04716CLF7A117D CRC64;				
Query Match	14.5%; Score 131.5; DB 1; Length 161;				
Best Local Similarity	25.2%; Pred. No. 0.031;				
Matches	39; Conservative 35; Mismatches 74; Indels 7; Gaps 4;				
QY	14 LLVANSAFADFPIGFVNSQSIAMESEAAKAQKLOQSEFGNEKTIQLEQAKDLOTKADD 73				
Db	12 LAMVTSQAQAD-KIAVNMGRLFQQVAQKTVGVSNTLENEPKGRAABLQKMBTDLSKMRQ 70				
QY	14 LLVANSAFADFPIGFVNSQSIAMESEAAKAQKLOQSEFGNEKTIQLEQAKDLOTKADD 73				
QY	74 LQKQSAAMSNGQARDKQREFELERNNFEKSRDFAIRVEQAENTLRQYLAEQYLAETI 133				
Db	71 LQSMFAGSD--RTKLEKDVMQSQTFAQRAQAFKEDRARRSNEEERNLVTRIQAVKVKV 127				
QY	134 AKKGKIKLVLDASGSVYMLEKNL-DITRKILEAI 167				
Db	128 ANDQSIDLVVD--ANTVAYNSSDVDFDITADVLKQV 160				
RESULT 10					
OMPH_CHLPN STANDARD;	PRTR;	171 AA.			
AC	Q9ZBNT;				
DT	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, fast annotation update)				
DE	OmpH-like protein precursor.				
GN	CNP0101 OR CP0457 OR CP070301 OR CPB0310.				
OS	Chlamydia pneumoniae (Chlamydophila pneumoniae).				
OC	Bacteria; Chlamydia; Chlamydiales; Chlamydiaceae; Chlamydophila.				
OK	NCBI_TaxID=83558;				

Qy	42	AKPAQKQLOSEFGNEKTIQLEKQARDILOTK--ADDLQKAAMSNSQAR-----EDKQ 90
Db	227	AQVQEVKLINHQELGAAQMKGQAEEALKASANADELRQKLVPAENVGHLKNTGEGLQ 284
Qy	91	REFPLERLNFEKEEKSRSRDFAIRYEQAEINTLROYLAEQIYLAETTAKEKGLKLVLDSAGSV 150
Db	287	KSTLLELRLSHLDQOVEEFLRKVEPYGETFNKALVQQV---EDLRQKLG--PLAGDVEGLH 344
Qy	151	MYLEKNL 157
Db	341	SFEBKDL 347
RESULT 12		
MFP1 LYCES		
ID	MFP1 LYCES	STANDARD;
AC	P93203;	PRT;
DT	16-OCT-2001 (Rel. 40, Created)	
DT	16-OCT-2001 (Rel. 40, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	MFP1 binding filament-like protein 1.	
GN	MFP1.	
OS	Lycopersicon esculentum (Tomato).	
OC	Rubidae; Viridiplantae; Streptophyta; Embryophytina; Tracheophytina;	
OC	Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; asterids;	
OC	Lamiidae; Solanales; Solanaceae; Solanum.	
OX	NCBI_TaxID=4081;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=CV; VENT CHERRY; TISSUE=Fruit;	
XX	MEDLINE=97112038; PubMed=8953774;	
RA	Meier I., Phelan T., Gruissew W., Spiker S., Schneider D.;	
RT	"MFP1, a novel plant filament-like protein with affinity for matrix attachment region DNA,"	
RT	Plant Cell 8:2105-2115 (1996).	
RL	-!- FUNCTION: Binds DNA. Interacts with chromatin via matrix attachment regions (MARS). Likely to participate in nuclear architecture by connecting chromatin with the nuclear matrix and potentially with the nuclear envelope.	
CC	-!- SUBCELLULAR LOCATION: Nuclear matrix.	
CC	-----	
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CC	-----	
DR	EMBL; Y07861; CAA69181..1; -.	
DR	DR PIR; T07111; T07111.	
KW	Nuclear protein; DNA-binding; Coiled coil.	
FT	COLLED COIL (POTENTIAL).	
FT	DOMAIN 125 681	
FT	DOMAIN 10 15	
SQ	SEQUENCE 697 AA; 79516 MW; 700A56D66A7B49 CRC64;	
Query Match 12.9% Score 116.5; DB 1; Length 697;		
Best Local Similarity 23.8%; Brd. No. 1..2; Mismatches 52; Indels 41; Gaps 0		
Qy	33 QSIAMESPAAKQKQK-----	--LOSEFGNEKTQLEKQAKDQTKA-- 71
Db	262 KEYLSRNTSKLAEEKEEVNSLSDMYQOSQDQMLNTSEIJKLKDQEJKRERELKCYS 322	
Qy	72 -DDLQKAAMSNSQAREDK-----QRFPLERLRNFEEKSRSRDFAIRVEQANTLROYLAE 124	
Db	322 EDLNVQNLNSLLIERDESKKELFAIQKEYSEFKNSDEKVADATIGEQ-EKRLHQ-LEE 371	
Qy	125 QI-----YLAETTAKEKGLKLVLDSAGSVTMYLEKQNDITKEILLE 165	
Db	380 QLTGTALESARNRSEVNLIAUDTREKENLRRMVDABLDVNKLKOBIEVQESLE 431	

RESULT	13
MYTH3_RAT	STANDARD; PRT; 1940 AA.
ID	MYTH3_RAT
AC	P12847;
DT	01-OCT-1989 (Rel. 12; Created) 01-OCT-1989 (Rel. 12; Last sequence update)
DT	15-MAR-2004 (Rel. 43; Last annotation update)
DB	Myosin heavy chain, fast skeletal muscle, embryonic.
GN	MYTH3.
OS	Rattus norvegicus (Rat).
OC	Karyotypic; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.
OC	NCBI_TAXID=10116;
OX	
RP	SEQUENCE FROM N.A. RN
RX	MEIDLINE-87050988; PubMed=3783701;
RA	Strehler E.E., Strehler-Page M.-A., Perriard J.C., Periasamy M., Nadal-Ginard B.;
RA	"Complete nucleotide and encoded amino acid sequence of a mammalian myosin heavy chain gene. Evidence against intron-dependent evolution of the rod." PT
RT	J. Mol. Biol. 190:291-317(1986).
CC	-!- FUNCTION: Muscle contraction.
CC	-!- SUBUNIT: Muscle myosin is a hexameric protein that consists of 2 heavy chain subunits (MHC), 2 alkali light chain subunits (MLC)
CC	and 2 regulatory light chain subunits (MLC-2).
CC	-!- SUBUNITARY LOCATION: Thick filaments of the myofibrils.
CC	-!- DOMAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils.
CC	-!- MISCELLANEOUS: Each myosin heavy chain can be split into 1 light meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be split further into 2 globular subfragments (S1) and 1 rod-shaped subfragment (S2).
CC	-!- SIMILARITY: Contains 1 myosin head domain.
CC	-!- SIMILARITY: Contains 1 IQ domain.
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CC	
DR	EMBL; X04267; CAA27817.1; -.
DR	PRTR; A24922; A24922.
DR	HSSPB; P13538; 2MYS.
DR	InterPro; IPR00048; IQ region.
DR	InterPro; IPR001609; myosin head.
DR	InterPro; IPR004009; Myosin_N.
DR	InterPro; IPR02928; Myosin_tail.
DR	InterPro; IPR002017; Spectrin.
DR	PFAM; PF00612; IQ; 2.
DR	PFAM; PF00663; myosin_head; 1.
DR	PFAM; PF02736; Myosin_N; 1.
DR	PRINTS; PRO0193; MIOSINHEAVY.
DR	ProDom; PD000355; myosin_head; 1.
DR	SMART; SM00015; IQ; 1.
DR	SMART; SM00242; MISC; 1.
DR	PROSITE; PS50096; IQ; 1.
KW	Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; Calmodulin-binding; Arg-binding; Methylation; MultiGene family.
KW	
FT	DOMAIN 1 781 MYOSIN HEAD-LIKE.
FT	DOMAIN 1 781 IQ.
FT	DOMAIN 1 811 COILED COIL (POTENTIAL).
FT	DOMAIN 1 840 1933 ATP (POTENTIAL).
FT	DOMAIN 1 179 186 ACTIN-BINDING.
FT	DOMAIN 1 656 678 ACTIN-BINDING.
FT	DOMAIN 1 758 772 ACTIN-BINDING.
FT	MOD RES 130 130 METHYLATION (TRI-) (POTENTIAL).
SO	SEQUENCE 1940 AA: 223857 MW: 85566A59EFS5A696 CRC64.

Query Match	12.4%;	Score 112.5;	DB 1;	Length 1940;		12.4%;	Score 112;	DB 1;	Length 173;
Best Local Similarity	25.4%;	Pred. No.	6.3;	Mismatches	51;	Indels	59;	Gaps	8;
Matches	49;	Conservative	34;						
QY	48 KLSQSEFGNEKTT--QLEKQAKDQLQTAKADDLQAK-SAAMSNGAREDKQR----- 91								
Db	1090 QLSQVDEDECILSLOLQQKTKELQARIEELTEEITAAERATRAKTEKQRSYAREEELSE 1149								
QY	92 -----EFLERNRNFEPEKSDFDFAIRVEQAENTLRYLAEDIYLIA 130								
Db	1150 RLEEAGGVTSTQIELNKGRKREAFKLKRDLFEAT---LOHEATVATLKKHADSAEELA 1205								
QY	131 ETI-----ARKKGKLVLDSASGSYMLEK---NLD-ITKEILEPAINAAWKGG 175								
Db	1206 EQIDNLQRVKQLEKEKSEFKLEIDLSSSYESVSKSKANLEKICRTLEDOLSEARGKNE 1265								
QY	176 S---KLPENAMRK 185								
Db	1266 ETQRSL-SLELTQK 1278								
RESULT 14									
OMPH_CHLMR	ID _OMPH_CHLMR STANDARD; PRT; 173 AA.								
AC	Q9Zn58 ;								
DT	28-FEB-2003 (Rel. 41, Created)								
DT	28-FEB-2003 (Rel. 41, Last sequence update)								
DT	28-FEB-2003 (Rel. 41, Last annotation update)								
DE	OmpH-like protein precursor.								
GN	CTP42.								
OS	Chlamydia trachomatis.								
BACTERIA; Chlamydia; Chlamydiales; Chlamydiaceae; Chlamydia.									
NCBI_TaxID=813;									
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=L2/434/Bu;								
RA	MEDLINE=9392470; PubMed=10463174;								
RA	Bannantine J.P., Rockey D.D.;								
RA	"Use of primate model system to identify Chlamydia trachomatis protein antigens recognized uniquely in the context of infection.";								
RL	Microbiology 145:2077-2085(1999).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=D/TW-3/Cx;								
RA	MEDLINE=90000059; PubMed=9784136;								
RA	Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger S., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.;								
RA	"Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";								
RA	Science 282:754-759(1998).								
CC	-!- SUBCELLULAR LOCATION: Outer membrane (Potential).								
CC	-!- SIMILARITY: BELONGS TO THE OMPH/HLPA FAMILY.								
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CC	EMBL; AF077009; AAC35946.1; -.								
CC	PIR; C71539; C71539.								
CC	InterPro; IPR005632; OmpH.								
CC	Pfam; PF03938; OmpH; 1.								
CC	Outer membrane; Signal; Complete proteome.								
DR	SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
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DR	FT SIGNAL 1 19 POTENTIAL.								
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DR	FT SIGNAL 1 19 POTENTIAL.								
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DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
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DR	FT SIGNAL 1 19 POTENTIAL.								
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DR	FT SIGNAL 1 19 POTENTIAL.								
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DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
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DR	FT SIGNAL 1 19 POTENTIAL.								
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DR	FT SIGNAL 1 19 POTENTIAL.								
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DR	FT SIGNAL 1 19 POTENTIAL.								
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DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.								
DR	FT CHAIN 20 173 MW; 6BB1574A6ABB82 CRC64;								
DR	FT SIGNAL 1 19 POTENTIAL.			</td					

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Db 6 LLSIMSLASSTVFAASSTNTIGIVNLLRCLESELGKCESAEFFKMKQFSNSTGMMEE 65
QY 64 AKDLOKADD----LOAKSAAMSNOAREDKOREFLEGRRNFEERKSRDFAIRVEQ---- 113
Db 66 LSSITISKLQDDDMGLESAAA-----ELRKKEEFLSEENTRAGQYRQI 111
QY 114 -AENTLR--QYLAEQYLAAETIAKKGLKLVIDSASGSYMLEKNDITKEILLEAINAA 170
Db 112 LNQNLLRMRMOKIMEAVRKASEVR1QEGLSALIN - EDIVLAIDFSSDKDAVIKILDDS 169
QY 171 WK 172
Db 170 FQ 171

Search completed: April 27, 2004, 09:36:11
Job time : 18 secs

QY	67	LQTAKADDLQAKSAMNSQAREDKOREFLLARRNFEKSDFAIRVEQAENTLRQYLAEGI	126	OX	[1]_TaxID=323;
DB	81	LKAMSDKLDKTAVIADSDETRRORELAAMDRLDFCRKOREFREDLNQRNEELAGVLLRA	140	RN	SEQUENCE FROM N.A.
RC				RP	
STRAIN	=DC3000;			RC	
RA	Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,			RA	
RA	Berry K., Utterback T., Van Aken S., Gwinn M.,			RA	
RA	Dobson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,			RA	
RA	Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,			RA	
RA	White O., Fraser C., Collier A.,			RA	"Complete sequence of <i>Pseudomonas syringae</i> ";
RT	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			RT	
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			RL	
DR	Q8BMH1; Q8BMH1; PRELIMINARY; PRT; 167 AA.			DR	InterPro; IPR005632; OmpH.
AC	Q8BMH1; DT 01-JUN-2003 (TREMBLrel. 24, Created)			DR	Pfam; PF03938; OmpH.
DT	01-UN-2003 (TREMBLrel. 24, Last sequence update)			KW	OMP OR PP1600.
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			SQ	Outer membrane protein OmpH.
DE					
GN					
OS	Pseudomonas putida (strain KT2440).				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;				
OC	Pseudomonadaceae; Pseudomonas.				
NCBI_TAXID	=16048;				
OX					
RN	SEQUENCE FROM N.A. MEDLINE=22423060; PubMed=12534463;			RESULT 4	
RX	Martins K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,			Q8VL03	
RA	Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,			ID	PRELIMINARY;
RA	Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,			AC	PRT; 191 AA.
RA	Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,			DT	OBV03;
RA	Chris Lee P., Holtzapple B., Scanlan D., Tran K., Moarzez A.,			DT	AC
RA	Utterback T., Rizzo M., Lee K., Kosack D., Noestl D., Wedler H.,			DT	01-MAR-2002 (TREMBLrel. 20, Created)
RA	Lauber J., Stipeancic D., Hoheisel J., Straetz M., Heim S.,			DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)
RA	Kirchitz C.M., Eisen J., Timmis K.N., Duersthoef A., Tuermmel B.,			DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)
RA	Fraser C.M.; "Complete genome sequence and comparative analysis of the			DE	DE
RT	metabolically versatile <i>Pseudomonas putida</i> KT2440.",			GN	Omp-like protein.
RL	Environ. Microbiol. 4:799-808(2002).			OS	Actinobacillus actinomycetemcomitans (Haemophilus
DR	EMBL; AE016779; AAC67221.1; -.			OS	actinomycetemcomitans)
DR	TIGR; PP1600; -.			OS	Bacterium; Gammaproteobacteria; Pasteurellales;
DR	InterPro; IPR005632; OmpH.			OC	Pasteurellaceae; Actinobacillus.
PFam	PF03938; OmpH; 1.			OX	
DR	Complete Proteome; SEQUENCE = 167 AA;			NCBI_TAXID	714;
GN	18809 MW; 02B7DBB4DA3ECFO CRC64;			RN	
DN				RP	SEQUENCE FROM N.A.
STRAIN				RC	STRAIN=ATCC 29523;
RA	Query Match 20 7%; Score 187 5; DB 16; Length 167;			RA	Hu W., Teng Y.-T.A.;
RA	Best Local Similarity 31.8%; Pred. No. 8.7e-06;			RA	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RA	Matches 54; Conservative 35; Mismatches 72; Indels 9; Gaps 4;			DR	EMBL; AF321231; RAU55890.1; -.
RA				DR	InterPro; IPR005632; OmpH; 1.
RA				DR	Pfam; PF03938; OmpH; 1.
RA				SQ	SEQUENCE 191 AA; 21491 MW; 2B812937C1573D02 CRC64;
RA				Query Match 18.8%; Score 170; DB 2; Length 191;	
RA				Best Local Similarity 28.8%; Pred. No. 0.00017;	
RA				Matches 55; Conservative 32; Mismatches 80; Indels 24; Gaps 4;	
RA					
QY	4 KTL5MAILACLVANSAFASDEPIGVFNQSITAMESSEAQAKQKLIQSERGNEKTO--L 60			QY	4 KTL5MAILACLVANSAFASDEPIGVFNQSITAMESSEAQAKQKLIQSERGNEKTO--L 63
DB	3 KLAQIAVVAAAVAVATPAP-ARMKVAVINYQVALLEDAAKKYAVDAEKKRSPQTLKSL 61			DB	3 KIVKQTKTALLSATLASSLAMDENAFISAYLFFNPDRKAVAEKLEAFKPTDKLAEN 62
RA	61 EKQAKDLQTADDLQKRSQAMSNOADEKOREFLLRNFBEKSDFAIRVEQANTLRQ 120			RA	AKDQLQTKADDLQ--AKSAMSNOA-----RE-----DKQREFPLIRRNF 101
RA	62 ESSAKGIQ--DRLIKGDGRNQQQERLEREFLFKQKARDFQFSKELENEAKAVADRMKL 118			RA	KKQIDTKTIAQKVEAKVALQDAPKURSADIKKREDEINKGNDQEEINKLIAEH 122
RA	121 YLAQBIQYLAETIAKKGKLVLYDASGSVMYLEKNULDITKEILEANNA 170			RA	PSPT0543.
RA	119 QLKPKLQDGAAEVTKKCGYDVL--RGAVIDVKVPQYDITRQVIERNNA 166			RA	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
RA				RA	Pseudomonadaceae; Pseudomonas.
RA				RA	
RESULT 3				RA	
Q886N4	Q886N4; PRELIMINARY; PRT; 167 AA.			RA	
AC	Q886N4; DT 01-JUN-2003 (TREMBLrel. 24, Created)			RA	
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)			RA	
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			DE	Outer membrane protein OmpH.
DE				GN	PSPT0543.
GN	Pseudomonas syringae (pv. tomato).			OS	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC				OC	Pseudomonadaceae; Pseudomonas.

Db	123 QKAKEFQNYAKRENEETEKLVAVSIQATNNVAKQKNTYLVDDR--SYYGMDGKNITE 180	Matches 44; Conservative 35; Mismatches 83; Indels 2; Gaps 1;
Qy	162 EIEEAINAWEK 172 181 EVLKAIPQAQ 191	4 KTLSMALLCIVANSASADFPIGVNSOSIAMESEAKAQKQLQSEGNEKTQLEKQ 63 3 KWLCAASGLALAASRVQA-AKIAIVNTSSIFQOLPARETVAQLENEFKGRATEQGM 61
Db	RESULT 5 005360 ID 005360; AC DT 01-JUL-1997 (TREMBurel. 04, Created) DT 01-OCT-1997 (TREMBurel. 04, Last sequence update) DT 01-OCT-2002 (TREMBurel. 22, Last annotation update) DE Autosome H. OS Yersinia enterocolitica. OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; OC Enterobacteriaceae; Yersinia. NCBI_TaxID=6101; RN [1] RP STRAIN FROM N.A. RC Sequence from N.A.: Freiburg strain 10543; RA Lauster R.; RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases. DR EMBL; Y12468; CAA30711.; - DR IntPro; IPR005612; OMPH. DR Pfam; PF03938; OmpH; 1. SQ SEQUENCE 164 AA; 1830 MW; 31A21F26BDFE317F CRC64;	64 AKDLOQTADDLQAKSAMSNQAREDQREFLELRNFEKSRSRDAIRVEQQANTLROYLA 123 62 ERDLOTKMQKLQRDGSTMRSQDRTEINDMKQRETFSTKQAEQQDNRRQMEERNKL 121
Query Match 18.4%; Score 166.5; DB 2; Length 164; Best Local Similarity 27.4%; Pred. No. 0.00025; Matches 45; Conservative 35; Mismatches 81; Indels 3; Gaps 2;	Qy 4 KTLSMALLCIVANSASADFPIGVNSOSIAMESEAKAQKQLQSEGNEKTQLEKQ 63 3 KWLCAASGLALAASRVQA-AKIAIVNTSSIFQOLPARETVAQLENEFKGRATEQGM 61 Db 64 AKDLOQTADDLQAKSAMSNQAREDQREFLELRNFEKSRSRDAIRVEQQANTLROYLA 123 62 ERDLOTKMQKLQRDGSTMRSQDRTEINDMKQRETFSTKQAEQQDNRRQMEERNKL 121	
Db	124 EQYI LAETIAETAKKGKLKVLDASGSVMYLEKLNLDITKEILEAI 167 122 SRIQDAIKVVGREGYDIVD--ANAVAYSVSKNITASVLKV 164	Qy 124 EOYI LAETIAETAKKGKLKVLDASGSVMYLEKLNLDITKEILEAI 167 Db 123 SRIQDAIKVVGREGYDIVD--ANAVAYSVSKNITASVLKV 164
RESULT 7 Q7WJ85 PRELIMINARY; PRT; 187 AA.		
Db	Q7WJ85 ID Q7WJ85; PRELIMINARY; PRT; 187 AA.	Qy 6 L5MALLCIVANSASF---SADPIGVNSOSIAMESPAKAQKQLQCLOSEFNBKTOLE 61 Db 24 VSLLAGALFGSSAVIAOQGTXGFUNTERLRESGPKAQSKIESEFKRDDELQ 83
SEQUENCE FROM N.A. STRAIN=RB50 / ATCC BAA-588; MEDLINE=22B22954; PubMed=12910271; RX Parkhill J., Sebaiha M., Preston A., Murphy L.D., Thomson N., Mungall K.L., RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L., RA Cedeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A., RA Achiman M., Atkin R., Baker S., Basham D., Basin N., Cherevach I., RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J., RA Feltwell T., Goble S., Hamlin N., Hauser H., Holroyd S., Jagels K., RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C., RA Rabinowitz B., Rutter S., Sanders M., Saunders D., Seeger K., RA Sharp S., Simmonds M., Skellern J.B., Squares R., Squars S., Stevens K., RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.; RT "Comparative analysis of the genome sequences of Bordetella pertussis, RT Bordetella parapertussis and Bordetella bronchiseptica." RL Nat. Genet. 35:32-40 (2003). DR EMBL; BI640444; CAE33107.1; -. RW Complete genome. SQ Sequence 187 AA; 20933 MW; AEC7F0C70785D0A7 CRC64;		
Query Match 17.8%; Score 161; DB 16; Length 187; Best Local Similarity 25.3%; Pred. No. 0.00071; Matches 42; Conservative 41; Mismatches 75; Indels 8; Gaps 2;		
Db	Qy 6 L5MALLCIVANSASF---SADPIGVNSOSIAMESPAKAQKQLQCLOSEFNBKTOLE 61 Db 24 VSLLAGALFGSSAVIAOQGTXGFUNTERLRESGPKAQSKIESEFKRDDELQ 83	Qy 62 KQANDLQTYADDLQAKSAMSNQOREDQREFLELRNFEKSRSRDAIRVEQQANTLROY 121 Db 84 RLSSLLRSQAEKFDRDAPVLSERVKRORLSIDMDLQRKREBFQEDNRNRNEFSS 143
RESULT 8 Q7VYCL PRELIMINARY; PRT; 187 AA.		
Db	Q7VYCL ID Q7VYCL; PRELIMINARY; PRT; 187 AA.	Qy 122 LAEQTYLAETIAETAKKGKLKVLDASGSVMYLEKLNLDITKEILEAI 167 Db 144 IVTRKANDAIKRIAESENQYDIIQDA---VTVNBRIDTQVDSL 185
SEQUENCE FROM N.A. STRAIN=Hm; RA Chatonet-Marton P.I., Givaudan A., Lanois A., Boemare N.E.; RT "Photorhabdus luminescens genomic region homologous to 4.0 minute RT Escherichia coli region promotes plasmidic phenotypes."; RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases. DR EMBL; AJ236920; CAB51930.1; -. DR IntPro; IPR005632; OmpH; 1. DR Pfam; PF03938; OmpH; 1. SQ SEQUENCE 165 AA; 18402 MW; 91BC8BE65FAD767 CRC64;		
Query Match 18.0%; Score 163; DB 2; Length 165; Best Local Similarity 26.8%; Pred. No. 0.00044;	Qy 122 LAEQTYLAETIAETAKKGKLKVLDASGSVMYLEKLNLDITKEILEAI 167 Db 144 IVTRKANDAIKRIAESENQYDIIQDA---VTVNBRIDTQVDSL 185	Qy 122 LAEQTYLAETIAETAKKGKLKVLDASGSVMYLEKLNLDITKEILEAI 167 Db 144 IVTRKANDAIKRIAESENQYDIIQDA---VTVNBRIDTQVDSL 185

DE Putative outer membrane protein.
 GN BP1428.
 OS Bordetella pertussis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetellales.
 NCBI_TAXID=520;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Tobama I / ATCC BAA-589 / NCTC 13251;
 RX MEDLINE=22827954; PubMed=12910271;
 RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
 Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 Cerdeno-Tarraga A.M., Temple L., James K., Harris P., Quail M.A.,
 Achtman M., Atkin R., Baker S., Basham D., Basam N., Cherevach I.,
 Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 Feltwell T., Goble A., Hamlin N., Hauber H., Holroyd S., Jagels K.,
 Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
 Rabinowitzsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
 Sharp S., Simmonds M., Skilton J., Squares R., Squares S., Stevens K.,
 Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,
 Bordetella parapertussis and Bordetella bronchiseptica.";
 RL Genet. 35:32-40 (2003).
 DR EMBL: BX640415; CAAE1718.1;
 KW Complete proteome.
 SQ SEQUENCE 187 AA; 20933 MW; A6C7F0C70785D0A7 CRC64;
 Query Match 17.8%; Score 161; DB 16; Length 187;
 Best Local Similarity 25.3%; Pred. No. 0.00078;
 Matches 42; Conservative 41; Mismatches 75; Indels 8; Gaps 2;
 -QY 6 LSMALLACLVANSFAF---SADFPVGNSQSAMESPAAKAQKLOSEFNEKTQLE 61
 -Db 24 VSLLAGALLFGSSAAVTAQGKTFGVTILERSGAKAQSKIEEFKRDDELQ 83
 -QY 62 KQAKDLOQTAKADDLQAKSAAMSQNQAREDKOREFELRNRFEKSRDFAIRVEQAENTLRQY 121
 -Db 84 RLSSLLRSQAERFDKDAPVLSSEDRVRQRRLNSLDQKRRFEEFSS 143
 -QY 122 LABQIYLAETIAKKGGKLIVLDSASGGSMYLERNIDITKELEAI 167
 -Db 144 IVTKANDAIKRIAEQNYDLIQDA ---VTVNPRTIDTKVIQSL 185

RESULT 9
 Q7WA51 PRELIMINARY; PRT; 203 AA.
 AC Q7WA51;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative outer membrane protein.
 GN BPP136.
 OS Bordetella parapertussis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetellales.
 NCBI_TAXID=519;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=12842 / ATCC BAA-587;
 RX MEDLINE=222627954; PubMed=12910271;
 RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
 Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 Achtman M., Atkin R., Baker S., Basham D., Basam N., Cherevach I.,
 Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 Feltwell T., Goble A., Hamlin N., Hauber H., Holroyd S., Jagels K.,
 Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
 Rabinowitzsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
 Sharp S., Simmonds M., Skilton J., Squares R., Squares S., Stevens K.,
 Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,
 Bordetella parapertussis and Bordetella bronchiseptica.";

RL Nat. Genet. 35:32-40 (2003).
 DR EMBL; BX404427; CAAE36838.1; -.
 KW Complete proteome.
 SQ SEQUENCE 203 AA; 22324 MW; 596E9D4EFF081D8 CRC64;
 Query Match 17.8%; Score 161; DB 16; Length 203;
 Best Local Similarity 25.3%; Pred. No. 0.00078;
 Matches 42; Conservative 41; Mismatches 75; Indels 8; Gaps 2;
 -QY 6 LSMALLACLVANSFAF---SADFPVGNSQSAMESPAAKAQKLOSEFNEKTQLE 61
 -Db 40 VSLLAGALLFGSSAAVTAQGKTFGVTILERSGAKAQSKIEEFKRDDELQ 99
 -QY 62 KQAKDLOQTAKADDLQAKSAAMSQNQAREDKOREFELRNRFEKSRDFAIRVEQAENTLRQY 122
 -Db 100 RLSSLLRSQAERFDKDAPVLSSEDRVRQRRLNSLDQKRRFEEFSS 159
 -QY 122 LABQIYLAETIAKKGGKLIVLDSASGGSMYLERNIDITKELEAI 167
 -Db 160 IVTKANDAIKRIAEQNYDLIQDA ---VTVNPRTIDTKVIQSL 201
 RESULT 10
 Q7VRD7 PRELIMINARY; PRT; 168 AA.
 ID Q7VRD7;
 AC Q7VRD7;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DE Histone-like protein, located in outer membrane.
 GN HLP_A; OR BFL280;
 OS Candidatus *Blochmannia floridanus*.
 OC Bacteriia; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; ant endosymbionts; *Candidatus Blochmannia*.
 NCBI_TAXID=203907;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22886019; PubMed=22886019;
 RA Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.,
 Latorre A., Russell C., Kamerbeek J., Gadau J., Hoelldobler B.,
 van Ham R.C.H.J., Gross R., Moya A.;
 RT "The genome sequence of *Blochmannia floridanus*: comparative analysis
 of reduced genomes";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393 (2003).
 DR EMBL: BX248585; CAB83351.1; -.
 KW Complete proteome.
 SQ SEQUENCE 168 AA; 19664 MW; 37BC6B37A5AAB43 CRC64;
 Query Match 16.8%; Score 152; DB 16; Length 168;
 Best Local Similarity 29.0%; Pred. No. 0.00777;
 Matches 49; Conservative 29; Mismatches 77; Indels 14; Gaps 5;
 -QY 1 MKVKTLISMAILCLVVANSAFASDPPIGVNSQSAMESPAAKAQKLOSEFNEKTQLE 60
 -Db 1 MCNRYMLGLIIWLAQINTYNAAN KIVMVNVANIFQOQAORTTEIKOLEYEFKDRRAEL 59
 -QY 61 EKQAKDLOQTAKADDLQAKSAAMSQNQAREDKOREFELRNRFEKSRDFAIRVEQAENTLRQ 120
 -Db 60 EMMERHDQTMQTLORDGATMATAIRNLEKSLAQRELESNKLF ---QQENHARQ 114
 -QY 121 ---YLAEOQYLAAETIAKKGGKLIVLDSASGGSMYLERNIDITKELEAI 163
 -Db 115 TEERDEKILDMLIVKTYNIACKENDIVID---TNAVYFFSSHIDTDV 161
 RESULT 11
 Q82U04 PRELIMINARY; PRT; 187 AA.
 ID Q82U04;
 AC Q82U04;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-Oct-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative transmembrane protein.

GN	NE1709.	Best Local Similarity 26.0%; Pred. No. 0.018;
OS	Nitrosomonas europaea.	Matches 38; Conservative 34; Mismatches 72; Indels 2; Gaps 1;
OC	Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;	
OC	Nitrosomonadaceae; Nitrosomonas.	
OX	[1]	
RN	RP	
RC	SEQUENCE FROM N.A.	
RA	STRAIN=ATCC 19718 / IFO 14298;	
RA	LINE=225841 ; PubMed=12100255;	
RA	Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,	
RA	Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,	
RA	Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.,	
RT	"Complete genome sequence of the ammonia-oxidizing bacterium and	
RT	obligate chemolithoautotroph Nitrosomonas europaea."	
RJ	J. Bacteriol. 185:2759-2773 (2003).	
RJ	ExBLR; BX31867; CAD85620.1; -.	
DR	GO:0016021; Cinterebral to membrane; IEA.	
DR	InterPro; IPR005632; CmpH.	
KW	Transmembrane Complete proteome.	
SQ	SEQUENCE 187 AA; 21976 MW; E5527AA431DBD42 CRC64;	
Query Match	Best Local Similarity 16.6%; Score 150.5; DB 16; Length 187;	
Matches 43; Conservative 39; Mismatches 88; Indels 13; Gaps 3;		
QY	3 VKTISMAILACIYANSAFSADPFTGVENSQISTAMESEAKAKQKLOSERFGNEKTQEK 62	
DB	17 VKAFVVTMFLPVHSSA -GEIKGVNTKEVLRRESPMAIEAQKIEREFQARDARRE 74	
QY	63 QAKDLOTAKKGLQAKSAMNSQAREDQREFLELRRNFEEKSRSRFAIRYQAENTLRYQI 122	
DB	75 LSAGITTAQELKNTGTVDEERKLKEPLLAGLSRQYRAQQCMREDISLRLRQEYKII 134	
QY	123 AEQTYLAETIAKKGLKLYLDASGSVYMLEKNDITKEILEAINAAMKGGSKLPPENA 182	
DB	135 LERINQVIRELAEKOSDILQLQDS -VYRSARIDTDQVKLNAR -----ESA 183	
QY	183 NRK 185	
DB	184 ARK 186	
RESULT 12	Best Local Similarity 25.1%; Score 137; DB 16; Length 171;	
ID	QBD2H1 PRELIMINARY; PRTR; 169 AA.	
AC	QBD2H1; 2003 (TREMBLrel. 23, Created)	
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)	
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
DE	H1PA protein.	
GN	H1PA OR WIGBR3830.	
OS	Wigglesworthia glossinidia brevipalpis.	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
OC	Enterobacteriaceae; Wigglesworthia.	
OX	[1]	
RN	SEQUENCE FROM N.A.	
RX	AKman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M., Aksoy S.; "Genome sequence of the endocellular obligate symbiont of tsetse flies, Wigglesworthia glossinidia."	
RT	Nat. Genet. 32:402-407(2002).	
RL	DB; AB03522; BAC24529.1; -.	
DR	InterPro; IPR005632; CmpH.	
DR	InterPro; IPR00437; Prok_lipoprot_S.	
DR	Pfam; PF03938; CmpH; 1.	
DR	PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.	
KW	Complete proteome.	
SQ	SEQUENCE 169 AA; 19677 MW; 6D78518E78D3CEFF6 CRC64;	
Query Match	15.5%; Score 140; DB 16; Length 169;	

[1] SEQUENCE FROM N.A.		SEQUENCE FROM N.A.		SEQUENCE FROM N.A.	
RP STRAIN=UC3;	RP STRAIN=UC3;	Q8EGG6; PubMed=10065039;	Q8EGG6; PubMed=10065023;	6 LISMALIACLLVANSFAADFPIGVNSQSIAAMESAAKAKQKLCLOSEFGNEKTKOLEKQAK 65	6 LISMALIACLLVANSFAADFPIGVNSQSIAAMESAAKAKQKLCLOSEFGNEKTKOLEKQAK 65
RC MEDLINE=99185023; PubMed=10065039;	RC MEDLINE=99185023; PubMed=10065023;	RA El-Ahdami W., Kyd J.M., Bastin D.A., Cripps A.W.;	RA El-Ahdami W., Kyd J.M., Bastin D.A., Cripps A.W.;	10 VTLALLGPAIAQAE----NIAVUDMGAVFEQLPOREQIMOSIKSERGDRMSEVORNQE 64	10 VTLALLGPAIAQAE----NIAVUDMGAVFEQLPOREQIMOSIKSERGDRMSEVORNQE 64
RT "Characterization of the gene encoding a 26-kilodalton protein (OMP26) from nontypeable Haemophilus influenzae and immune responses to the recombinant protein.";	RT "Characterization of the gene encoding a 26-kilodalton protein (OMP26) from nontypeable Haemophilus influenzae and immune responses to the recombinant protein.";	RT NON TER 195 AA; 21448 MW; AFAA0C0375C91615 CRC64;	RT NON TER 195 AA; 21448 MW; AFAA0C0375C91615 CRC64;	66 DLQKADDLQAKSAMSNQAREDKQREFLELRNFEKSR--DEAIRVEAVENTLROYLA 123	66 DLQKADDLQAKSAMSNQAREDKQREFLELRNFEKSR--DEAIRVEAVENTLROYLA 123
RT recombinant protein.";	RT recombinant protein.";	RT DR EMBL; AF109088; AAD23970.1; -.	RT DR EMBL; AF109088; AAD23970.1; -.	65 EMRSLMEKQRDGGLMNTQKTEVRKQALKSYQNGKAUJEDLRQGB--QNKL 122	65 EMRSLMEKQRDGGLMNTQKTEVRKQALKSYQNGKAUJEDLRQGB--QNKL 122
RT Infect Immun. 67:1935-1942 (1999).	RT Infect Immun. 67:1935-1942 (1999).	DR InterPro; IPR005632; OmpH.	DR InterPro; IPR005632; OmpH.	124 EQYIYLAETTAKKGLLYIDSAGGSVMYLEKNDITKILEAN 168	124 EQYIYLAETTAKKGLLYIDSAGGSVMYLEKNDITKILEAN 168
FT Pfam; PF03938; OmpH; 1.	FT Pfam; PF03938; OmpH; 1.	DB 123 VRVQKANTIAERKVDLVQ--RGAVIVVKPNADISGKVVEAHL 165	DB 123 VRVQKANTIAERKVDLVQ--RGAVIVVKPNADISGKVVEAHL 165		
SEQUENCE 195 AA;	SEQUENCE 195 AA;				
Query Match Score 15.0%; Best Local Similarity 27.7%; Matches 54; Conservative 33; Mismatches 33; Indels 76; Gaps 6;	Query Match Score 15.0%; Best Local Similarity 27.7%; Matches 54; Conservative 33; Mismatches 33; Indels 76; Gaps 6;	Search completed: April 27, 2004, 09:37:04 Job time : 41 secs	Search completed: April 27, 2004, 09:37:04 Job time : 41 secs		
Q8EGG6; ID Q8EGG6; AC Q8EGG6; DT 01-MAR-2003 (TRMBLrel. 23, Created) 01-MAR-2003 (TRMBLrel. 23, Last sequence update) 01-JUN-2003 (TRMBLrel. 24, Last annotation update)	Q8EGG6; ID Q8EGG6; AC Q8EGG6; DT 01-MAR-2003 (TRMBLrel. 23, Created) 01-MAR-2003 (TRMBLrel. 23, Last sequence update) 01-JUN-2003 (TRMBLrel. 24, Last annotation update)	62 KQAKULQTK---ADDLQAKSAMSNQAREDKQ----REFLELRNFE 102	62 KQAKULQTK---ADDLQAKSAMSNQAREDKQ----REFLELRNFE 102	62 ASKKEYDDKTAARKREAKVAALEXDAPIRLQROBEINKLGAAADELOLMQE 121	62 ASKKEYDDKTAARKREAKVAALEXDAPIRLQROBEINKLGAAADELOLMQE 121
Q8EGG6; DE Outer membrane Protein OmpH. GN OR SO1638. OS Shewanella oneidensis. CC Alteromonadaceae; Gammaproteobacteria; Alteromonadales; CC Alteromonadales; Shewanellia. NCBI_TaxID=708631; RN [1]	Q8EGG6; DE Outer membrane Protein OmpH. GN OR SO1638. OS Shewanella oneidensis. CC Alteromonadaceae; Gammaproteobacteria; Alteromonadales; CC Alteromonadales; Shewanellia. NCBI_TaxID=708631; RN [1]	103 KSRDFAIRVERAENTRQ----YLAEQYIYLAETTAKKGLLYIDSAGGSVMYLEKNL 157	103 KSRDFAIRVERAENTRQ----YLAEQYIYLAETTAKKGLLYIDSAGGSVMYLEKNL 157	122 --QDKKVVQEFAQNQEERKQAAERKGKLDISIQTATNNIAKACYTYVLD--ANSVVFAYEGK 177	122 --QDKKVVQEFAQNQEERKQAAERKGKLDISIQTATNNIAKACYTYVLD--ANSVVFAYEGK 177
Q8EGG6; DR 158 DITKETLEATAAAWK 172	Q8EGG6; DR 158 DITKETLEATAAAWK 172	178 DITEEVLKSIPEAK 192	178 DITEEVLKSIPEAK 192		
RESULT 15	RESULT 15	PRELIMINARY; PRT; 168 AA.	PRELIMINARY; PRT; 168 AA.		
Q8EGG6; ID Q8EGG6; AC Q8EGG6; DT 01-MAR-2003 (TRMBLrel. 23, Created) 01-MAR-2003 (TRMBLrel. 23, Last sequence update) 01-JUN-2003 (TRMBLrel. 24, Last annotation update)	Q8EGG6; ID Q8EGG6; AC Q8EGG6; DT 01-MAR-2003 (TRMBLrel. 23, Created) 01-MAR-2003 (TRMBLrel. 23, Last sequence update) 01-JUN-2003 (TRMBLrel. 24, Last annotation update)	DE Outer membrane Protein OmpH.	DE Outer membrane Protein OmpH.	GN	GN
RC Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seibadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beaman M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Rutherford K., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khorri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Ventur J.C., Nealson K.H., Fraser C.M.; RT "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis."	RC Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seibadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beaman M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Rutherford K., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khorri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Ventur J.C., Nealson K.H., Fraser C.M.; RT "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis."	RT RL EMBL; AE015609; AAN54693.1; -.	RT RL EMBL; AE015609; AAN54693.1; -.	DR TIGR; SO1638; -.	DR TIGR; SO1638; -.
RC Nelson W.C., Read T.D., Eisen J.A., Seibadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beaman M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Rutherford K., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khorri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Ventur J.C., Nealson K.H., Fraser C.M.; RT "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis."	RC Nelson W.C., Read T.D., Eisen J.A., Seibadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beaman M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Rutherford K., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khorri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Ventur J.C., Nealson K.H., Fraser C.M.; RT "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis."	DR InterPro; IPR005632; OmpH.	DR InterPro; IPR005632; OmpH.	DR Pfam; PF03938; OmpH; 1.	DR Pfam; PF03938; OmpH; 1.
RC Complete proteome.	RC Complete proteome.	SEQUENCE 168 AA; 18992 MW; 86622927EF3A12956 CRC64;	SEQUENCE 168 AA; 18992 MW; 86622927EF3A12956 CRC64;	SQ	SQ
RC	RC	Query Match Score 15.0%; Best Local Similarity 23.6%; Pred. No. 0.038;	Query Match Score 15.0%; Best Local Similarity 23.6%; Pred. No. 0.038;		

GenCore version 5.1.6
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OM protein - protein search, using sw mode1

Run on: April 27, 2004, 09:31:28 ; Search time 59 Seconds
(without alignments)
890.743 Million cell updates/sec

Title: US-10-018-290A-1
Perfect score: 904
Sequence: 1 MKVKTLSTMAILCLVVANSA.....INAIAWKGGSKLPPEANRKK 186

Scoring table: BLOSUM62
GapOp 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Maximum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04;*
1: GeneseqP1980s;*
2: GeneseqP1990s;*
3: GeneseqP2000s;*
4: GeneseqP2001s;*
5: GeneseqP2002s;*
6: GeneseqP2003as;*
7: GeneseqP2003bs;*
8: GeneseqP2004s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89.5	98.8	187	AAB37887	Aab37887 Lawsonia
2	89.5	17.6	166	ABM67564	Abm67564 Photorhabd
3	134.5	14.9	197	AAW10221	Aaw10221 Haemophil
4	134	14.8	166	AYY75115	Aay75115 Neisseria
5	133	14.7	166	AYY75116	Aay75116 Neisseria
6	131	14.5	166	AYY75114	Aay75114 Neisseria
7	131	14.5	171	AAE04724	Aae04724 Chlamydia
8	131	14.5	171	ABB94317	Abb94317 Chlamydia
9	131	14.5	171	ABB9054	Abb9054 Chlamydia
10	131	14.5	185	ABP80503	Abp80503 N. gonorr
11	131	14.5	185	ABP79763	Abp79763 N. gonorr
12	127.5	14.1	484	ABP30015	Abp30015 Streptococ
13	118.5	13.1	382	AAB90663	Aab90663 Human sec
14	118	13.1	158	2	AAY34897
15	118	13.1	717	3	AAB21231 Tomato Le
16	116	12.8	177	2	AAY32170
17	115.5	12.8	170	2	AAY34497
18	115.5	12.8	174	2	AAY34496
19	115.5	12.8	177	2	AAY34370
20	111.3	12.5	195	3	AAB21229 Tomato E-
21	111.3	12.5	1957	6	ABM68633
22	112.5	12.4	876	3	AAY77573
23	112.5	12.4	876	4	AAU28104
24	112	12.4	173	5	ABB94352
25	112	12.4	173	7	ADD43762

ALIGNMENTS

RESULT 1	
ID	AAB37887
ID	AAB37887 standard; protein; 187 AA.
XX	
AC	AAB37887;
XX	
DT	06-MAR-2001 (first entry)
XX	
DE	Lawsonia intracellularis OmpH.
XX	
KW	Lawsonia intracellularis; OmpH; immunogen; antigen; vaccine;
KW	avian infection; porcine infection; porcine proliferative enteropathy;
KW	PPE.
XX	
OS	Lawsonia intracellularis.
PN	WO200069905-A1.
XX	
PD	23-NOV-2000.
XX	
PP	11-MAY-2000; 2000WO-AU000438.
XX	
PR	13-MAY-1999; 99US-0133986P.
XX	
(PGR-) PIG RES & DEV CORP.	
PA (AGPL-) AGRIC VICTORIA SERVICES PTY LTD.	
XX	
PI	Hasse D, Panaccio M, Sinistaj M;
XX	
DR	WPI; 2001-016211/02.
DR	N-PSDB; AAC89304.
XX	
PT	New isolated Lawsonia spp. OmpH polypeptides and nucleic acids useful for the prophylaxis, treatment and detection of Lawsonia infections.
XX	
PS	Claim 6; Page 81-82; 85pp; English.
XX	
CC	The present sequence is Lawsonia intracellularis OmpH. Immunogenic OmpH peptides and polypeptides are useful as antigens in a vaccine preparation for conferring humoral immunity against Lawsonia intracellularis and related pathogens in animal hosts. The polypeptides are capable of eliciting the production of antibodies against Lawsonia sp. when administered to an avian or porcine animal. The OmpH polypeptides and polynucleotides can be used for the detection, prophylaxis and treatment of an infection of an animal by Lawsonia sp. They are used particularly for porcine proliferative enteropathy (PPE) infections
CC	
CC	Sequence 187 AA;
SQ	

Query Match 98.8%; Score 893.5; DB 4; Length 187;
 Best Local Similarity 99.5%; Pred. No. 6.Se-72;
 Matches 186; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MKYKTLSMAILACIVANSFAADFPIGYENSIAMSEAAKAOKCLOSEGNEKSQL 60
 Db 1 MKYKTLSMAILACIVANSFAADFPIGYENSIAMSEAAKAOKCLOSEGNEKSQL 60
 XX sequence represents one of the isolated P. luminescens proteins

Qy 61 EKQAKDLDQTAKDLQAKSAMSNQAREDQREFELRNFEKSRDFEAIRVEAENTRQ 120
 Db 61 EKQAKDLDQTAKDLQAKSAMSNQAREDQREFELRNFEKSRDFEAIRVEAENTRQ 120

Qy 121 YLAQIYLAETIAKKKGKLVLDSASGSVYMLEKLNLTKELEAN -AANRKGGSSLP 179
 Db 121 YLAQIYLAETIAKKKGKLVLDSASGSVYMLEKLNLTKELEANAAAWKXGGSSLP 180

Qy 180 EMANRKK 186
 Db 181 EMANRKK 187

RESULT 2
 ABM67564 standard; protein; 166 AA.
 AC ABM67564;
 XX 20-NOV-2003 (first entry)
 DE Photorhabdus luminescens protein sequence #661.
 KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
 KW detection; food; gene expression; plant; animal; microorganism; toxin;
 KW antibiotic; biopesticide; virulence factor; disease model; plague;
 KW whooping cough.
 OS Photorhabdus luminescens.
 PN WO200294867-A2.
 XX 28-NOV-2002.
 PD XX
 FF 07-FEB-2002; 2002WO-1B003040.
 PR XX
 07-FEB-2001; 2001FR-00001659.

PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Duchaud E, Tacourt S, Glaser P, Frangeul L, Kunst F, Danchin A;
 PI Buchrieser C;
 XX
 DR WPI; 2003-148459/14.

XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
 PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
 XX
 PS Claim 2; SEQ ID NO 661; 1205pp; French.
 XX
 CC The invention relates to the isolation of genes and their encoded
 CC proteins from Photorhabdus luminescens. The isolated sequences are
 CC sources of probes and primers for detecting the genome of P. luminescens
 CC and related species; to study polymorphisms; for gene analysis and for
 CC detection/amplification of the genes. Antibodies (Ab) raised against the
 CC polypeptides encoded by the genes are used for detection/identification
 CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
 CC carry a gene-containing vector are used to select compounds that
 CC modulate, regulate, induce or inhibit expression of the genes in plants,
 CC animals or microorganisms other than P. luminescens and are able to alter
 CC responses or sensitivity to toxins and antibiotics produced by P.
 CC luminescens. Cells transformed to express the genes are useful for
 CC recombinant production of the proteins, particularly toxins and

CC antibiotics useful as insecticides, bactericides and fungicides. The
 CC genes, proteins, vectors containing the genes and Ab are also useful
 CC therapeutically (to treat microbial infection by bacteria or fungi that
 CC are sensitive to P. luminescens encoded toxins or antibiotics) and as
 CC biopesticides. Other uses of the genes and the proteins are as virulence
 CC factors and for identifying targets of human diseases for which P.
 CC luminescens is a model (particularly plague and whooping cough). This
 CC sequence represents one of the isolated P. luminescens proteins
 XX

Sequence 166 AA;
 SQ Query Match 17.6%; Score 159; DB 6; Length 166;
 Best Local Similarity 26.8%; Pred. No. 2.5e-06;
 Matches 44; Conservative 34; Mismatches 84; Indels 2; Gaps 1;

Qy 4 KILSMMAILACLLIVANSFASADFTIGVENSQSTAMESEAAKAOKCLOSEGNEKTOLEKQ 63
 Db 3 KULCAASRGIALAFSGVQAADDKIAVNGEFLFQLQPLPAREAVYKQLENEFKNASELORM 62

Qy 64 ARDQTQKADDLQAKSAMSNQAREDKQREFELRNFEKSRDFEAIRVEAENTRQYL 123
 Db 63 ETDIQSKIQKLQDQGSTMKSSENTNLKEVKGLVLDASGSVYMLEKLNLTKELEAN 167

Qy 124 EQTYLAAETTAKEKKGLVLDASGSVYMLEKLNLTKELEAN 167
 Db 123 SRIDQAIKVAGKEDGYDVID- ANAVAYSVSGKNITTSVLRQV 164

RESULT 3
 AAU10221 standard; protein; 197 AA.
 ID AAU10221;
 XX AC AAU10221;
 DE 02-JUL-1997 (first entry)
 DT 02-JUL-1997
 XX Haemophilus influenzae outer membrane protein OMP26.
 DE XX
 KW Vaccine; outer membrane protein; OMP26; respiratory tract; otitis media.
 OS XX
 HS Haemophilus influenzae.
 OS XX
 FH Key Location/Qualifiers
 Peptide 1..23
 FT /label= signal
 FT Protein 24..197
 FT /label= OMP26
 XX WO9701638-A1.
 XX PD 16-JAN-1997.
 XX PD 27-JUN-1996; 96WO-GB001549.
 XX PR 27-JUN-1995; 95GB-0013074.
 XX (CORT-) CORTECS INT LTD.
 PA XX
 PI Kyd J, Cripps A, Smith CJ;
 XX DR WPI; 1997-102029/09.
 DR N-PSDB; AAT50939.
 XX PT New antigenic outer membrane protein from Haemophilus influenzae - useful
 PT in vaccines and as diagnostic reagent.
 XX PA Claim 2; Fig 1; 34pp; English.
 XX The present sequence represents the novel protein, outer membrane protein
 CC OMP26 from Haemophilus influenzae. This new antigenic protein can be used
 CC as an immunogen in vaccines for the treatment or prevention of H.
 CC influenzae infections (of the respiratory tract or otitis media), and as
 CC a diagnostic reagent for diagnosing such infections. OMP26 if isolated

CC from the NTHI-I strain of *H. influenzae*, protects against infection by CC homologous and heterologous strains

XX Sequence 197 AA;

Query Match 14.9%; Score 134.5; DB 2; Length 197;
Best Local Similarity 26.8%; Pred. No. 0.00047;
Matches 56; Conservative 34; Mismatches 78; Indels 41; Gaps 7;
Qy 2 KVKTLSMAILACLLVANSFAFADDPFGVNSQSTAMEBAAAKAQKKESEFGENEKTQE 61
Db 6 KVTAALAGI---ALASGTAASEKIAKFAINAGY FQHJDROAVADKDAEFPVAFKIA 61
Qy 62 KQAKDLQTK---ADDLQKSAAMNSNQREDQ-----REFFLRNRNEE 102
Db 62 ASKVEVDKIAAARKKVKVEKAALKDAPRQLRADIQRQBEINKLGAAEDALQKLME 121
Qy 103 KSRDFAIRVEQAENTLQQ----YLAEOYIYLAETIAKKGKLVLVDSASGSYMTLEKNL 157
Db 122 --QDKKVKVEFQAQNEMKRAQABERGKLLDQSQTATNNLARAKGTYVLD--ANSVVFAYEGK 177
Qy 158 DITKEBILAINAAMWKGSSKULPEMANRKK 186
Db 178 DITEEEVKSIPAS -----EKAQEK 197

RESULT 4

AAY75115

ID AAY75115 standard; protein; 166 AA.

AC AAY75115;

XX 21-MAR-2000 (first entry)

XX Neisseria meningitidis ORF 570 protein sequence SEQ ID NO:1704.

XX Neisseria meningitidis; Neisseria gonorrhiae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
KW antibacterial; gene therapy.

XX Neisseria meningitidis.

XX 11-NOV-1999.

XX 30-APR-1999; 99WO-US009346.

XX 01-MAY-1998; 98US-0083758P.

PR 31-JUL-1998; 98US-0094869P.

PR 02-SEP-1998; 98US-0098994P.

PR 09-OCT-1998; 98US-0099062P.

PR 09-OCT-1998; 98US-0103749P.

PR 09-OCT-1998; 98US-0103794P.

PR 25-FEB-1998; 98US-0103798P.

PR 25-FEB-1998; 98US-0121528P.

PA (CHIR) CHIRON CORP.

PA (GENO-) INST GENOMIC RES.

XX DR 2000-062150/05.

DR N-PSDB; AAZ53877.

XX Fraser C, Galeotti C, Grandi G, Hickey E, Masiognani V, Mora M; Peter森 J, Pizza M, Rappuoli R, Ratti G, Scallato E, Scarcelli M; Tettelin H, Venter JC;

XX DR WPI; 2000-062150/05.

DR N-PSDB; AAZ53878.

CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides CC and polypeptides. AAZ54537 to AAZ54616 to AAZ55473 represent CC PCR primers used in the exemplification of the present invention. The CC polypeptides, the polynucleotides, antibodies and compositions of the CC invention can be used as vaccines, as diagnostic reagents, and as CC immunogenic compositions. The polypeptides can be used as medicaments for treating or preventing infection due to *Neisseria* CC bacteria (e.g., meningitis, and septicemia), to detect the presence of CC *Neisseria* bacteria, or to raise antibodies. They may also be used to CC screen for agonists or antagonists, which may themselves have use as CC antibacterial agents. The polynucleotides of the invention may also be CC used in gene therapy protocols

XX

Sequence 166 AA;

Query Match 14.8%; Score 134; DB 3; Length 166;
Best Local Similarity 27.3%; Prod. No. 0.00042;
Matches 48; Conservative 39; Mismatches 63; Indels 26; Gaps 8;
Qy 4 KTLSMAILACLLVANSFAFADDPFGVNSQSTAMESERAAKAOKLQSEFGNEKTQLEKQ 63
Db 6 RAPAAFLGLCCTAGAHDTFKQGFINTERYLESKARKTQTLDEFSARQDELQK- 64
Qy 64 AKDLQTADDLQAKSA-----AMSNOAREDQKOR----EFLFLRNFEKSRSRDEFAIRVEQ 113
Db 65 ---LQREGUDLERQLAEGLRNLNAKKAQ-A-EKWPRLVYAAFRKQQAQFEE---DYNLRNRE 117

RESULT 5

AAY75116

ID AAY75116 standard; protein; 166 AA.

XX AAY75116;

AC AAY75116;

XX DT 21-MAR-2000 (first entry)

XX

Neisseria meningitidis ORF 570 protein sequence SEQ ID NO:1706.

XX

DE

XX

KW

Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;

KW

antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;

KW

antibacterial; gene therapy.

XX

Neisseria meningitidis.

XX

OS

XX

PN

W09957280-A2.

XX

PN

W09957280-A2.

XX

DE

XX

W099572

PCT PT PT PT PT PT
XX XX XX XX XX XX
Novel Neisserial polypeptides predicted to be useful antigens for
vaccines and diagnostics.

Claim 2: Page 877; 1453PP; English.

AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY759
represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
and polypeptides AAZ54537 to AAZ54576 and AAZ55473 re-
PCR primers used in the exemplification of the present invention.
polypeptides, the polynucleotides, antibodies and compositions of
invention can be used as vaccines, diagnostics, and as
immunogenic compositions. The polypeptides can be used in the manu-
of medicaments for treating or preventing infection due to Neisser-
bacteria (e.g. meningitis and septicaemia), to detect the presence
Neisseria bacteria, or to raise antibodies. They may also be used
screen for agonists or antagonists, which may themselves have use
antibacterial agents. The polynucleotides of the invention may also
used in gene therapy protocols

Sequence 166 AA:
SQ

Query	Match	14.7%	Score	133;	DB	3;	Length	166;
Best Local Similarity	25.9%	Pred. No.	0.00052;					
Matches 48;	Conservative	32;	Mismatches	61;	Indels	44;	Gaps	7;
Qy	4 KTLSMALLACLLVANSASAESADPFIGVENSQSITAMESEAAKAAQKKLQSEFGNKTQLKQ	63						
Db	6 RAFAAALIGLGLCCTTAGAHADTFQKIGFINTERIYLESKGARKTQKTLDESEFAAQDELQK-	64						
Qy	64 ARDLQTKADDLQKSA-----AMSNQRE-----DKRCRFE-----LRRNFEKS	104						
Db	65 ---LQRIGLDLRLERQLAESKLDAKKAQDEEKWGLVAAPRKKGQAQFEEDYLNRRN---	116						
Qy	105 RDEFARVEQAENTLRRQYLAEQIYLAETIAKKKGKLVLIDSASGSVMMYLEKNLDITKEIL	164						
Db	117 BEFASTQCONANRVIK-----IAKQGYDVIIQ---DVIYNTNTQDVTDSVI	160						
Qy	165 EAINA	1.69						
Db	161 KEMADA	1.65						

RESULT 6
AAV75114 standard; protein; 166 AA.
ID AAV75114

XX AAY75114;
AC XX 12-SEP-2003 (revised)
DT DT 21-MAR-2000 (first entry)
XX

De Neisseria gonorrhoeae ORF 570 protein sequence SEQ ID NO:1102.
 XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
 KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
 KW antibacterial; gene therapy.

OS Neisseria gonorrhoeae.

WO9957280-A2.
PN 17 NOV 1 0000
DD

כט ברכות ובראשונה

THE JOURNAL OF CLIMATE VOL. 11, NO. 1, JANUARY 1998

PR 01-MAI-1998; 98US-0083-58P.
PR 31-JUL-1998; 98US-0094869P.

PR 02-SEP-1998; 98US-0098994P.
PB 02-SEP-1998; 98US-00989962P.

PR 09-OCT-1998; 98US-0103749P.

PR 09-OCT-1998; 98US-0103796P.

ER 25-FEB-1999; 9905-01215ZBP.

Page 5

XX	(AVET) AVENTIS PASTEUR LTD.	PA	Fling SP, Skeiky YAW, Probst P, Bhatia A;
XX	XX	XX	WPI: 2002-17901/23.
PI	Murdin AD, Oomen RP, Wang J, Dunn P;	XX	Novel compositions comprising Chlamydia Cap1 protein and its use in the treatment of Chlamydia infection.
DR	WPI: 2001-418020/44.	XX	Chlamydia outer membrane protein and corresponding DNA molecules for preventing, diagnosing and treating Chlamydia infection in mammals, such as humans.
DR	N-PSDB; AAD9313.	XX	Claim 16; Fig 1; 74pp; English.
PT	PT	XX	The present sequence is Chlamydia pneumoniae outer membrane protein. The outer membrane protein is useful for preventing, treating and detecting Chlamydia infection in humans. The outer membrane protein DNA is useful for producing the encoded polypeptide and in the construction of attenuated Chlamydia strains that can over express the polynucleotide or express a non-toxic, mutated form. It is also used as vaccine. The probes for outer membrane protein are useful in diagnostic tests by capture or detection probes and the primers are useful in diagnostic methods involving PCR. The antibody against outer membrane protein is useful for purifying the outer membrane protein. (Updated on 11-SEP-2003 to standardise OS field)
PS	PS	XX	Sequence 171 AA;
XX	XX	XX	Query Match 14.5%; Score 131; DB 4; Length 171;
XX	XX	XX	Best Local Similarity 22.7%; Pred. No. 0.00081;
XX	XX	XX	Matches 37; Conservative 44; Mismatches 76; Indels 6; Gaps 3;
Qy	14 LIVVANSFAADFPIGVNSQSIAAMESAAKAAQKQLQS--EFGNEKTLQLEKQAKDLQTQ 70	Db	14 LIVVANSFAADFPIGVNSQSIAAMESAAKAAQKQLQS--EFGNEKTLQLEKQAKDLQTQ 70
Qy	10 LLVLGSTSAAHNLGYTNLKRCLLESIDLGKRTTEELFAMKQQFVKNAEKIEELTSIYK 69	Db	10 LLVLGSTSAAHNLGYTNLKRCLLESIDLGKRTTEELFAMKQQFVKNAEKIEELTSIYK 69
Qy	71 ADDLQAQSAAMSNGAREDQKFETFLRNFEKSRDFAIRVEQENTLRQYLAQIYLLA 130	Db	71 ADDLQAQSAAMSNGAREDQKFETFLRNFEKSRDFAIRVEQENTLRQYLAQIYLLA 130
Qy	70 LQD-EDYMESSLSDASSEELRKKEFEDLSSEYNAQSQYQSTIQNSVNRKLIQEVKIAA 128	Db	70 LQD-EDYMESSLSDASSEELRKKEFEDLSSEYNAQSQYQSTIQNSVNRKLIQEVKIAA 128
Qy	131 ETIAKKKGSLKLVIDSASSGSMYKLEKNLDITKEILEAINAAWKK 173	Db	131 ETIAKKKGSLKLVIDSASSGSMYKLEKNLDITKEILEAINAAWKK 173
Qy	129 ESVRSKEKLEATINEE- -AVLATAPGTDKTTETIAILNESFKK 169	Db	129 ESVRSKEKLEATINEE- -AVLATAPGTDKTTETIAILNESFKK 169
RESULT 9			
ABB90564			
ID	ABB90564	standard, protein;	171 AA.
XX	XX	XX	XX
AC	AC	AC	AC
DT	29-AUG-2003	(revised)	DT 29-AUG-2003 (revised)
XX	XX	XX	XX
DE	Chlamydia pneumoniae cp65577 protein,	SEQ ID NO: 77.	DE Chlamydia pneumoniae cp65577 protein, SEQ ID NO: 77.
XX	XX	XX	XX
KW	Chlamydial infection; antigen; immunogen; vaccine; diagnosis;		KW Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KW	human respiratory disease; cardiovascular disease; atherosclerosis;		KW human respiratory disease; cardiovascular disease; atherosclerosis;
KW	coronary artery disease; carotid artery stenosis; myocardial infarction;		KW coronary artery disease; carotid artery stenosis; myocardial infarction;
KW	cerebrovascular disease; aortic aneurysm; claudication; stroke;		KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW	brain CWL019.		KW brain CWL019.
XX	XX	XX	XX
OS	Chlamydophila pneumoniae.		OS Chlamydophila pneumoniae.
XX	XX	XX	XX
FN	FN	Location/Qualifiers	FN Location/Qualifiers
FT	FT	1..21	FT 1..21
FT	FT	Signal_peptide	FT Signal_peptide
PD	PD	22..171	PD 22..171
FT	FT	/note= "Mature protein"	FT /note= "Mature protein"
XX	XX	XX	XX
PN	PN		PN WO200202606-A2.
PR	PR		PR WO200202606-A2.
PR	PR		PR 10-JAN-2002.
XX	XX	XX	XX
PF	PF		PF 03-JUL-2001; 2001WO-1B001445.
(CORI-X CORIXA CORP.			(CORI-X CORIXA CORP.
XX	XX	XX	XX

PR	03-JUL-2000;	2000GB-00016363.	PN	WO200279243-A2.
PR	11-JUL-2000;	2000GB-00017047.	XX	XX
PR	21-JUL-2000;	2000GB-00017983.	PD	10-OCT-2002.
PR	07-AUG-2000;	2000GB-00019368.	XX	XX
PR	18-AUG-2000;	2000GB-00020440.	PF	12-FEB-2002; 2002WO-IB002069.
PR	14-SEP-2000;	2000GB-00022583.	XX	XX
PR	10-NOV-2000;	2000GB-00027549.	PR	12-FEB-2001; 2001GB-00003424.
PR	22-DEC-2000;	2000GB-00031706.	XX	XX
PA	(CHIR-) CHIRON SPA.	PA	(CHIR-) CHIRON SPA.	
XX		XX		
PI	Ratti G, Grandi G;	PI	Fontana MR, Pizza M,	Masignani V, Monaci E;
XX		XX		
DR	WPI; 2002-154726/20.	DR	WPI; 2003-050415/05.	
DR	N-PSDB; AB191222.	DR	N-PSDB; ABZ41473.	
XX		XX		
PT	Novel Chlamydia pneumoniae protein useful in the manufacture of a medicament for treatment or prevention of infection due to Chlamydia, preferably Chlamydia pneumoniae, and for diagnostic purposes.	PT	New Protein from <i>Neisseria gonorrhoeae</i> , useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection.	
PT		XX		
PS	Claim 1; Page 78; 364PP; English.	PS	Disclosure; Page 737; 815PP; English.	
PS		XX		
CC	Sequences ABB0526-ABB0715 represent novel proteins from Chlamydia pneumoniae (strain CWL029), and AB191184-AB191373 represent DNA encoding them. The proteins are predicted to be immunogenic and may therefore be useful in vaccine production and for diagnostic purposes. Chlamydia pneumoniae is a common cause of respiratory disease in humans, and is also involved in the development of cardiovascular diseases such as atherosclerosis, coronary artery disease, carotid artery stenosis, myocardial infarction, cerebrovascular disease, aortic aneurysm, claudication and stroke. The proteins and nucleic acids of the invention may be used in vaccines and pharmaceutical compositions for the prevention or treatment of chlamydial infections, particularly Chlamydia pneumoniae infections. The proteins may also be used in the detection of Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched DNA probe assay or blotting techniques for determining Chlamydia pneumoniae gene expression. The present sequence represents a specifically claimed Chlamydia pneumoniae protein of the invention. (Updated on 29-AUG-2003 to standardise OS field)	CC	The present invention relates to proteins from <i>Neisseria gonorrhoeae</i> . Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to or antibody is useful for the comprising the protein, nucleic acid or antibody is useful for the manufacture of medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention	
CC		CC		
SQ	Sequence 171 AA;	SQ	Sequence 185 AA;	
Query Match	14.5%;	Query Match	14.5%;	
Best Local Similarity	29.8%;	Best Local Similarity	29.8%;	
Matches	53;	Matches	53;	
CC	Conservative	CC	Conservative	
CC	34;	CC	34;	
CC	Mismatches	CC	Mismatches	
CC	61;	CC	61;	
CC	Indels	CC	Indels	
CC	30;	CC	30;	
CC	Gaps	CC	Gaps	
CC	10;	CC	10;	
QY	6 LSMALLACH-LVANSANSAFADF-PIGVENSONSIAMESEAAKAAQKKLOSEFGNEKTQLE 61	QY	62 KQARDLQTKRADDIQAQSA-----AMSGNAREDQREFELRR---NPBEKSDFDFAIV 111	
Db	1:	Db	1:	
Db	23 LTRAPAAALIGLCCTTGAHADTFKXGIFTNTTERYLESKOARNIQKLTDGEFSARQDELQ 82	Db	83 K---LQREGLDLRQLAGSKLKAQKAA-EEWKRGIVAFRAKQAOQPE--DYNDLR 134	
Db		Db		
QY	112 EQAENTILRQYLAQTYLAETIAAKKKGLKLVLDASGSYMYLEKKNLDITKEILEFAINA 169	QY	112 EQAENTILRQYLAQTYLAETIAAKKKGLKLVLDASGSYMYLEKKNLDITKEILEFAINA 169	
Db	1:	Db	1:	
Db	135 NEEFASLQQN-ANRIVV--KIAKQEGXDVILQ---DVLYVNTOYDVTDSVTCMNA 184	Db	135 NEEFASLQQN-ANRIVV--KIAKQEGXDVILQ---DVLYVNTOYDVTDSVTCMNA 184	
Db		Db		
RESULT 11		RESULT 11		
ID	ABP79763	ID	ABP79763	
AC		AC		
XX		XX		
OS		OS		
Neisseria gonorrhoeae.		Neisseria gonorrhoeae.		
XX		XX		
PN		PN		
W0200279243-A2.		W0200279243-A2.		
XX		XX		
PD		PD		
XX		XX		
PF		PF		
XX		XX		
PR		PR		
XX		XX		
12-FEB-2001;		12-FEB-2001;		
2001GB-00003424.		2001GB-00003424.		
XX		XX		
(CHIR-) CHIRON SPA.		(CHIR-) CHIRON SPA.		
XX		XX		
PA		PA		
XX		XX		
Fontana MR, Pizza M,		Fontana MR, Pizza M,		
Masignani V, Monaci E;		Masignani V, Monaci E;		
PI		PI		

XX WPI; 2003-050415/05.
 DR N-PSDB; ABZ40733.
 XX
 PT New protein from *Neisseria gonorrhoeae*, useful for the manufacture of a medicament for treating or preventing *N. gonorrhoeae* infection.
 PS Disclosure; Page 629; 815pp; English.
 XX
 CC The present invention relates to proteins from *Neisseria gonorrhoeae*.
 CC Antibodies that specifically bind to the proteins, the composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing *N. gonorrhoeae* infection, this may be in the form of a vaccine or gene therapy.
 CC Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention
 XX Sequence 185 AA;
 SQ Query Match 14.5%; Score 131; DB 6; Length 185;
 Best Local Similarity 29.8%; Pred. No. 0.0009;
 Matches 53; Conservatives 34; Mismatches 61; Indels 30; Gaps 10;
 XX
 QY 6 LSWAILACI--LVANSAFSADE--PIGVENSQSIAMESAAKAKQKLQSEFGNEKTQE 61
 Db 23 LTRFAAATLGLCCTTGAAATFQIGFINTERYLESCOARNQTKDGEFSARQDEQ 82
 QY 62 KQAKDLOQKADDLOAKSA----AMSNQAREDKOREFELLRR---NFEKEKSPDFARV 111
 Db 83 K----LREQDLERQLAGGKLDKAKKAA-EEKWRLVEAFKKQAAFF--DYNIRR 134
 QY 112 EQAENTLROYLAECIYLAAFTIAKKGKGLVLDASGSYMLEKRNLDITKELEAINA 169
 Db 135 NEEFASLQON-ANRVIV--KIAKOBGVDLQ---DVLYANTQYDVIDSVIKEMNA 184
 -RESULT 12
 ABP30015 ID ABP30015 standard; protein; 484 AA.
 AC ABP30015;
 XX 02-JUL-2002 (first entry)
 DE Streptococcus polypeptide SEQ ID NO 9206.
 XX
 KW Streptococcus; GAS; GBS; group B streptococcus; *Streptococcus agalactiae*; Group A *Streptococcus*; *Streptococcus pyogenes*; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
 KW Streptococcus pyogenes.
 OS WO200234771-A2.
 PN 02-MAY-2002.
 XX
 PP 29-OCT-2001; 2001WO-GB004789.
 PR 27-OCT-2000; 2000GB-00026333.
 PR 24-NOV-2000; 2000GB-00028727.
 PR 07-MAR-2001; 2001GB-00005640.
 XX
 PA ((CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 Telford J., Masiognani V., Margarit Y RosI, Grandi G., Fraser C.;
 PI Tettelin H.;
 DR WPI; 2002-352536/38.
 XX
 PT New Streptococcus protein for the treatment or prevention of infection or

XX disease caused by *Streptococcus* bacteria, such as meningitis, and for detecting a compound that binds to the protein.
 XX
 PT Claim 1; Page 4044; 4525pp; English.
 PS
 CC The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A *streptococcus/GAS* (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (1), nucleic acids encoding (1), ABN6044-ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by *Streptococcus* bacteria, particularly *S. agalactiae* and *S. pyogenes*. Nucleic acids encoding (1) are used to detect *Streptococcus* in a biological sample. (1) is used to determine whether a compound binds to (1). A composition comprising (1) or a nucleic acid encoding (1), may be used as a vaccine or diagnostic composition. The disease caused by (1) is prevented or treated may be meningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity chromatography, immunoassays, and distinguishing/identifying *Streptococcus* proteins
 XX
 SQ Sequence 484 AA;
 Query Match 14.1%; Score 127.5; DB 5; Length 484;
 Best Local Similarity 25.3%; Pred. No. 0.006;
 Matches 49; Conservative 27; Mismatches 77; Indels 41; Gaps 6;
 QY 2 KVVKLMSMIALACIUVANSAFSADEPPI---GVENQSQTAMESEAAAQAQKKLQSEFGNE-- 56
 Db 14 KLKNGTAGTASAVAVLTVLGAGFANQTEVKANGDNREVITEDLAANNPATONIRLRYENKDL 73
 QY 57 -----KTOLEKQADLQTAADDLOAKSAAMSQNQREDKORE 92
 Db 74 KARLENAMEVAGRDGFKAEELEKAKQALEDQRDLETKLQELQDYDLAKESTSWDRQR- 132
 QY 93 FLEIIRRNFBEKSDFIAFREQAEINTLROYLAETIAKKGKGLVLDASAS--GS 149
 Db 133 --LEKELEKKKALELLAIDQASRDYHRTA---LEKELEKKKALELLAIDQASRDYHRTA 185
 QY 150 VMYIIEKNLD-DITKE 162
 Db 186 ANVLEKELELTITE 199
 XX
 RESULT 13
 ABP90663 ID ABP90663 standard; protein; 382 AA.
 AC ABP90663;
 XX 01-JUN-2001 (first entry)
 DE Human secreted protein, SEQ ID NO: 206.
 XX
 KW Human; secreted protein; immunomodulatory; antischlerotic; dermatological; antiinflammatory; anti-HIV; cyostatic; cardiant; vascular; anti-angiogenic; ophthalmological; neuroprotectant; nootropic; anticonvulsant; antialzheimers; antiparkinsonian; antimicrobial; vulnerary; vaccine; gene therapy; cancer; protein coordinate data; infection.
 XX
 OS Homo sapiens.
 PN WO200121658-A1.
 PD 22-SEP-2000; 2000WO-US026013.
 XX
 PR 24-SEP-1999; 99US-0155709P.
 XX

DR N-PSDB; AAA95812.
 XX
 PR Nucleic acid fragments from tobacco, corn, soybean and rice, encoding
 PR proteins that are homologs to the MAR binding filament-like protein 1
 XX (MFP1), useful for development of novel phenotypes.

PS Claim 5; Page 54-56; 62pp; English.

XX The present sequence is LaMFP1, the matrix attachment region (MAR)
 CC binding filament-like protein 1 (MFP1) from tomato. MFP1 has features of
 CC a novel anchor protein that most likely connects chromatin via MAR DNA
 CC with the nuclear envelope and nuclear filament proteins. MFP1 nucleic
 CC acids and proteins may be used to better understand the mechanisms
 CC underlying this process so that the attachment of transgenes to the
 CC nuclear matrix may be used routinely to improve gene expression. They may
 CC be used to study MFP1 expression, leading to the creation of novel
 CC developmental phenotypes that may be beneficial for crop growth and
 CC development. In addition, if the reduction in expression of one of the
 CC genes leads to a growth or developmental defect in the plant, this gene
 CC can be used as a novel herbicide target.

XX Sequence 717 AA;

	Query Match	Score	Length
Best Local Matches	13.1%	118	3
Similarity	22.7%	Pred. No. 0.069;	
Conservative	40;	Mismatches	53;
Matches	39;	Indels	40;
		Gaps	5;
Oy	33 QSIAMESAAKAAQKK-	-----	71
Db	262 KEVSURNTSKLAERKESEVNSLSDMYQQSQDQLMNLTSKELKDEIQRRERELELKCVS	-----	321
Oy	72 -DDILOQAKSAMSNQAREDK-----	QREFTELRNFEKSRDFAIRVEAENTTRQYIAE	124
Db	322 EDNINVQLNSLLERDESKKELHAIQKESEFKNSDEKVASDKLKGQEKRIHQ-LEE	-----	380
Oy	125 QI-----YIAAETIAKKKGKLVLDASGSMVYLEKNLDITKSLIE	-----	165
Db	381 QLGTAALSEASRNVEILLADLTREKENLRMVDALDNVNKLQEIEVTVQSLE	-----	432

Search completed: April 27, 2004, 09:35:42
 Job time : 61 secs